



## SEQUENCE LISTING

<110> Duvick, Jonathan P.  
Gilliam, Jacob T.  
Maddox, Joyce R.  
Rao, Aragula Gururaj  
Crasta, Oswald R.  
Folkerts, Otto

<120> Amino Polyol Amine Oxidase Polynucleotides and Related Polypeptides and Methods of Use

<130> 1134R

<140> US 09/658,835

<141> 2000-09-08

<150> US 60/092,936

<151> 1998-07-25

<150> US 60/135,391

<151> 1999-05-21

<150> US 09/352,159

<151> 1999-07-12

<150> US 09/352,168

<151> 1999-07-12

<160> 53

<170> PatentIn version 3.1

<210> 1

<211> 372

<212> DNA

<213> Exophiala spinifera

<220>

<221> misc\_feature

<222> (346)..(346)

<223> n = A, T, C, or G

<400> 1		
gggccccggc gttctcgtag gctgcgcgga gttggtccca gacagacttt tgtcgatcc		60
gcttggactg ttgggaccac ttccgtcccc ggtctccgac catgaaacag gtaatggacc		120
attgtcgatc gacgtcgatg ctggtatctc tggcaaatga gatgggtca cagctcgatt		180
ggaggacgcc cgagaagcct tggtcgcc accacggctt gtcccatacg aagactatct		240
tgctatagta gcccaggata gaattttccg ccaatgcttg cttctcgccg ggaagaggtg		300
gtgaaaatgt caaggtggta tacaaggttt tcggtaacga aaccancacc ttttgcttc		360
ggaacacggc gc		372

<210> 2  
 <211> 182  
 <212> DNA  
 <213> Exophiala spinifera

<400> 2  
 gaattttccg ccaatgcttg cttctcgccg ggaagaggtg gtgaaaatgt caagggtggga 60  
 tacaagggttgcgtaacga aaccaccacc ttttgcttc ggaacacggc gcccgaggcc 120  
 gatcgactg tacagccgga tgccgactgc tcaatttcag cgacgggggt gttgaggtgc 180  
 ac 182

<210> 3  
 <211> 29  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Designed oligonucleotide for 3' RACE N21965

<400> 3  
 tggtttcgtt accgacaacc ttgtatccc 29

<210> 4  
 <211> 28  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Designed oligonucleotide for 5' RACE 21968

<400> 4  
 gagttggtcc cagacagact tttgtcgt 28

<210> 5  
 <211> 1389  
 <212> DNA  
 <213> Exophiala spinifera

<220>  
 <221> CDS  
 <222> (1)..(1386)  
 <223>

<400> 5  
 gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg 48  
 Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly Leu  
 1 5 10 15

gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt 96  
 Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu  
 20 25 30

gag	gcg	atg	gat	cgt	gta	ggg	gga	aag	act	ctg	agc	gta	caa	tcg	ggt	144
Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	
35					40					45						
ccc	ggc	agg	acg	act	atc	aac	gac	ctc	ggc	gct	gcg	tgg	atc	aat	gac	192
Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	
50					55					60						
agc	aac	caa	agc	gaa	gta	tcc	aga	ttg	ttt	gaa	aga	ttt	cat	ttg	gag	240
Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	
65					70					75				80		
ggc	gag	ctc	cag	agg	acg	act	gga	aat	tca	atc	cat	caa	gca	caa	gac	288
Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	
85					90					95						
ggt	aca	acc	act	aca	gct	cct	tat	ggt	gac	tcc	ttg	ctg	agc	gag	gag	336
Gly	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu		
100					105					110						
gtt	gca	agt	gca	ctt	gcg	gaa	ctc	ctc	ccc	gta	tgg	tct	cag	ctg	atc	384
Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	
115					120					125						
gaa	gag	cat	agc	ctt	caa	gac	ctc	aag	gcg	agc	cct	cag	gcg	aag	cgg	432
Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	
130					135					140						
ctc	gac	agt	gtg	agc	tcc	gcg	cac	tac	tgt	gag	aag	gaa	cta	aac	ttg	480
Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	
145					150					155				160		
cct	gct	gtt	ctc	ggc	gta	gca	aac	cag	atc	aca	cgc	gct	ctg	ctc	ggt	528
Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	
165					170					175						
gtg	gaa	gcc	cac	gag	atc	agc	atg	ctt	ttt	ctc	acc	gac	tac	atc	aag	576
Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	
180					185					190						
agt	gcc	acc	ggt	ctc	agt	aat	att	ttc	tcg	gac	aag	aaa	gac	ggc	ggg	624
Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	
195					200					205						
cag	tat	atg	cga	tgc	aaa	aca	ggt	atg	cag	tcg	att	tgc	cat	gcc	atg	672
Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	
210					215					220						
tca	aag	gaa	ctt	gtt	cca	ggc	tca	gtg	cac	ctc	aac	acc	ccc	gtc	gct	720
Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	
225					230					235				240		
gaa	att	gag	cag	tcg	gca	tcc	ggc	tgt	aca	gta	cga	tcg	gcc	tcg	ggc	768
Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	
245					250					255						
gcc	gtg	tcc	cga	agc	aaa	aag	gtg	gtg	gtt	tcg	tta	ccg	aca	acc	ttg	816
Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	
260					265					270						

tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca		864	
Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala			
275	280	285	
ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta		912	
Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val			
290	295	300	
tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa		960	
Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln			
305	310	315	320
tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc		1008	
Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val			
325	330	335	
gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cg		1056	
Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg			
340	345	350	
aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac		1104	
Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp			
355	360	365	
caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg		1152	
Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro			
370	375	380	
gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga		1200	
Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly			
385	390	395	400
gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg		1248	
Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser			
405	410	415	
gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg		1296	
Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr			
420	425	430	
tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa		1344	
Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln			
435	440	445	
cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag		1389	
Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala			
450	455	460	

<210> 6  
<211> 462  
<212> PRT  
<213> Exophiala spinifera

<400> 6

Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly Leu			
1	5	10	15

Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu  
20 25 30

Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly  
35 40 45

Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp  
50 55 60

Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu  
65 70 75 80

Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp  
85 90 95

Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu  
100 105 110

Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile  
115 120 125

Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg  
130 135 140

Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu  
145 150 155 160

Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly  
165 170 175

Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys  
180 185 190

Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly  
195 200 205

Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met  
210 215 220

Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala  
225 230 235 240

Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly

245

250

255

Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu  
260 265 270

Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala  
275 280 285

Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val  
290 295 300

Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln  
305 310 315 320

Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val  
325 330 335

Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg  
340 345 350

Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp  
355 360 365

Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro  
370 375 380

Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly  
385 390 395 400

Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser  
405 410 415

Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr  
420 425 430

Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln  
435 440 445

Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
450 455 460

<210> 7

<211> 1442

<212> DNA

<213> Exophiala spinifera

<220>  
<221> CDS  
<222> (1)..(645)  
<223>

<220>  
<221> Intron  
<222> (646)..(698)  
<223>

<220>  
<221> CDS  
<222> (699)..(1439)  
<223>

<400> 7  
gac aac gtt gcg gac gtg gta gtg gtc ggc gct ggc ttg agc ggt ttg 48  
Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu  
1 5 10 15  
  
gag acg gca cgc aaa gtc cag gcc ggc ggt ctg tcc tgc ctc gtt ctt 96  
Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu  
20 25 30  
  
gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt 144  
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly  
35 40 45  
  
ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac 192  
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp  
50 55 60  
  
agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag 240  
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu  
65 70 75 80  
  
ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac 288  
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp  
85 90 95  
  
ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag 336  
Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu  
100 105 110  
  
gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc 384  
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile  
115 120 125  
  
gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cg 432  
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg  
130 135 140  
  
ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg 480  
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu  
145 150 155 160  
  
cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt 528  
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly

165	170	175	
gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys 180	185	190	576
agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly 195	200	205	624
cag tat gtg cga tgc aaa aca ggtcgctgtg gtgtcgcttc aggtggggga Gln Tyr Val Arg Cys Lys Thr 210	215		675
ctcgtttctc agtggtcatt cca ggt atg cag tcg att tgc cat gcc atg tca Gly Met Gln Ser Ile Cys His Ala Met Ser 220		225	728
aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu 230	235	240	776
att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala 245	250	255	824
gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr Leu Tyr 260	265	270	872
ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu 275	280	285	920
gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp 290	295	300	968
gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser 310	315	320	1016
agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp 325	330	335	1064
cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys 340	345	350	1112
tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln 355	360	365	1160
ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala 370	375	380	1208
aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct			1256

Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala			
390	395	400	
ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg			1304
Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala			
405	410	415	
ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct			1352
Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser			
420	425	430	
tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga			1400
Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg			
435	440	445	
ggg gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag			1442
Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala			
450	455	460	
<210> 8			
<211> 462			
<212> PRT			
<213> Exophiala spinifera			
<400> 8			
Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu			
1	5	10	15
Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu			
20	25	30	
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly			
35	40	45	
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp			
50	55	60	
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu			
65	70	75	80
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp			
85	90	95	
Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu			
100	105	110	
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile			
115	120	125	

Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg

130 135 140

Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu  
145 150 155 160

Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly  
165 170 175

Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys  
180 185 190

Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly  
195 200 205

Gln Tyr Val Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met  
210 215 220

Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala  
225 230 235 240

Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly  
245 250 255

Ala Val Phe Arg Ser Lys Val Val Val Ser Leu Pro Thr Thr Leu  
260 265 270

Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala  
275 280 285

Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val  
290 295 300

Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln  
305 310 315 320

Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val  
325 330 335

Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg  
340 345 350

Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp  
355 360 365

Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro  
370 375 380

Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly  
385 390 395 400

Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser  
405 410 415

Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr  
420 425 430

Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln  
435 440 445

Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
450 455 460

<210> 9

<211> 458

<212> PRT

<213> Exophiala spinifera

<400> 9

Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu  
1 5 10 15

Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu  
20 25 30

Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly  
35 40 45

Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp  
50 55 60

Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu  
65 70 75 80

Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp  
85 90 95

Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu  
100 105 110

Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile  
115 120 125

Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg  
130 135 140

Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu  
145 150 155 160

Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly  
165 170 175

Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys  
180 185 190

Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly  
195 200 205

Gln Tyr Val Arg Cys Lys Thr Gly Ala Cys Gly Val Val Ser Gly Gly  
210 215 220

Gly Leu Val Ser Gln Trp Ser Phe Gln Val Cys Ser Arg Phe Ala Met  
225 230 235 240

Pro Cys Gln Arg Asn Leu Phe Gln Ala Gln Cys Thr Ser Thr Pro Pro  
245 250 255

Ser Leu Lys Leu Ser Ser Arg His Pro Ala Val Gln Tyr Asp Arg Pro  
260 265 270

Arg Ala Pro Cys Ser Glu Ala Lys Arg Trp Trp Phe Arg Tyr Arg Gln  
275 280 285

Pro Cys Ile Pro Pro His Phe His His Leu Phe Pro Pro Arg Ser Lys  
290 295 300

His Trp Arg Lys Ile Leu Ser Trp Ala Thr Ile Ala Arg Ser Ser Tyr  
305 310 315 320

Gly Thr Ser Arg Gly Gly Ala Asn Lys Ala Ser Arg Ala Ser Ser Asn  
325 330 335

Arg Ala Val Thr Pro Ser His Leu Pro Glu Ile Pro Ala Ser Thr Ser  
340 345 350

Ile Asp Asn Gly Pro Leu Pro Val Ser Trp Ser Glu Thr Arg Asp Gly  
355 360 365

Ser Gly Pro Asn Ser Pro Ser Arg Tyr Asp Lys Ser Leu Ser Gly Thr  
370 375 380

Asn Ser Ala Gln Pro Thr Arg Thr Pro Gly Pro Lys Ser Gln Ser Arg  
385 390 395 400

Pro Thr Cys Ser Lys Ser Ser Gly Arg Ser Ser Ser Ile Ser Lys Glu  
405 410 415

Leu Arg Ala Pro Ser Met Gly Thr Ile Ser Ser His Trp Val Arg Arg  
420 425 430

Ser Glu Arg Arg Ser Arg Val Phe Ile Ser Leu Glu Arg Arg Arg Leu  
435 440 445

Phe Gly Lys Gly Ile Trp Lys Gly Pro Tyr  
450 455

<210> 10  
<211> 1392  
<212> DNA  
<213> Exophiala spinifera

<220>  
<221> CDS  
<222> (1)..(1389)  
<223>

<220>  
<221> misc\_feature  
<222> (1)..(3)  
<223> Extra lysine in K:trAPAO

<400> 10  
aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt 48  
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly  
1 5 10 15

ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt 96  
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val  
20 25 30

ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg 144  
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser  
35 40 45

ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat		192	
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn			
50	55	60	
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg		240	
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu			
65	70	75	80
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa		288	
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln			
85	90	95	
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag		336	
Asp Gly Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu			
100	105	110	
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg		384	
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu			
115	120	125	
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag		432	
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys			
130	135	140	
cg <sup>g</sup> ctc gac agt gt <sup>g</sup> agc tt <sup>c</sup> g <sup>c</sup> g <sup>c</sup> cac tac tgt gag aag gaa cta aac		480	
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn			
145	150	155	160
tt <sup>g</sup> cct gct gtt ctc g <sup>g</sup> c <sup>g</sup> a <sup>a</sup> c <sup>a</sup> c <sup>a</sup> g <sup>a</sup> at <sup>c</sup> a <sup>c</sup> c <sup>g</sup> c <sup>g</sup> q <sup>c</sup> c <sup>t</sup> g <sup>c</sup>		528	
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu			
165	170	175	
ggt gt <sup>g</sup> gaa gcc cac gag atc agc at <sup>g</sup> ctt tt <sup>c</sup> ctc acc gac tac atc		576	
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile			
180	185	190	
aag agt gcc acc ggt ctc agt aat att tt <sup>c</sup> tc <sup>g</sup> gac aag aaa gac g <sup>g</sup> <sup>c</sup>		624	
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly			
195	200	205	
gg <sup>g</sup> cag tat at <sup>g</sup> cga t <sup>g</sup> c <sup>a</sup> g <sup>a</sup> g <sup>g</sup> t <sup>g</sup> at <sup>g</sup> c <sup>a</sup> g <sup>t</sup> tc <sup>g</sup> att t <sup>g</sup> c <sup>a</sup> t <sup>g</sup> c <sup>g</sup>		672	
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala			
210	215	220	
at <sup>g</sup> t <sup>c</sup> a <sup>a</sup> g <sup>g</sup> a <sup>c</sup> c <sup>t</sup> g <sup>t</sup> c <sup>a</sup> g <sup>g</sup> t <sup>c</sup> g <sup>c</sup> c <sup>a</sup> c <sup>c</sup> c <sup>c</sup> g <sup>t</sup> c <sup>c</sup>		720	
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val			
225	230	235	240
gct gaa att gag cag tc <sup>g</sup> g <sup>c</sup> t <sup>c</sup> g <sup>g</sup> t <sup>g</sup> t <sup>a</sup> g <sup>t</sup> c <sup>a</sup> t <sup>g</sup> g <sup>c</sup> t <sup>c</sup> g <sup>c</sup>		768	
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser			
245	250	255	
gg <sup>c</sup> g <sup>c</sup> g <sup>t</sup> t <sup>c</sup> c <sup>a</sup> g <sup>c</sup> a <sup>a</sup> a <sup>a</sup> g <sup>t</sup> g <sup>t</sup> g <sup>t</sup> t <sup>c</sup> g <sup>t</sup> t <sup>a</sup> c <sup>c</sup> a <sup>c</sup> a <sup>c</sup>		816	
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr			
260	265	270	
tt <sup>g</sup> t <sup>a</sup> t <sup>c</sup> c <sup>c</sup> a <sup>c</sup> t <sup>t</sup> g <sup>a</sup> t <sup>c</sup> t <sup>t</sup> t <sup>c</sup> c <sup>c</sup> g <sup>c</sup> g <sup>a</sup> a <sup>a</sup> c <sup>a</sup>		864	
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln			
275	280	285	

gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc		912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe		
290	295	300
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc		960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu		
305	310	315
320		
caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac		1008
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp		
325	330	335
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga		1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly		
340	345	350
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg		1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp		
355	360	365
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag		1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu		
370	375	380
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa		1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln		
385	390	395
400		
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt		1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly		
405	410	415
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag		1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu		
420	425	430
445		
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt		1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly		
435	440	445
460		
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag		1392
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala		
450	455	460
<210> 11		
<211> 463		
<212> PRT		
<213> Exophiala spinifera		
<220>		
<221> misc_feature		
<222> (1)..(3)		
<223> Extra lysine in K:trAPAO		
<400> 11		
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly		

1

5

10

15

Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val  
20 25 30

Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser  
35 40 45

Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn  
50 55 60

Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu  
65 70 75 80

Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln  
85 90 95

Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu  
100 105 110

Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu  
115 120 125

Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys  
130 135 140

Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn  
145 150 155 160

Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu  
165 170 175

Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile  
180 185 190

Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly  
195 200 205

Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala  
210 215 220

Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val  
225 230 235 240

Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser

245

250

255

Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr

260

265

270

Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln

275

280

285

Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe

290

295

300

Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu

305

310

315

320

Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp

325

330

335

Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly

340

345

350

Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp

355

360

365

Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu

370

375

380

Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln

385

390

395

400

Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly

405

410

415

Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu

420

425

430

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly

435

440

445

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala

450

455

460

<210> 12

<211> 34

<212> DNA

<213> Artificial

<220>

<223> Primer sequence designed for cloning DNA into expression vectors,  
N23256

<400> 12  
gggaaattca aagacaacgt tgccgacgtg gtag

34

<210> 13

<211> 34

<212> DNA

<213> Artificial

<220>

<223> Primer sequence designed for cloning DNA into expression vectors  
N23256

<400> 13  
ggggcggccg cctatgctgc tggcaccagg ctag

34

<210> 14

<211> 29

<212> DNA

<213> Artificial

<220>

<223> Designed oligonucleotide for 3' RACE, N21965

<400> 14  
tggttcggtt accgacaacc ttgtatccc

29

<210> 15

<211> 28

<212> DNA

<213> Artificial

<220>

<223> Designed oligonucleotide for 5' RACE, N21968

<400> 15  
gagtttgtcc cagacagact ttgtcgt

28

<210> 16

<211> 1673

<212> DNA

<213> Exophiala spinifera

<220>

<221> sig\_peptide

<222> (1)..(267)

<223> yeast alpha mating factor secretion signal

<220>

<221> CDS  
<222> (1)..(1662)  
<223>

<400> 16  
atg aga ttt cct tca att ttt act gct gtt tta ttc gca gca tcc tcc 48  
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser  
1 5 10 15  
  
gca tta gct gct cca gtc aac act aca aca gaa gat gaa acg gca caa 96  
Ala Leu Ala Ala Pro Val Asn Thr Thr Glu Asp Glu Thr Ala Gln  
20 25 30  
  
att ccg gct gaa gct gtc atc ggt tac tca gat tta gaa ggg gat ttc 144  
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe  
35 40 45  
  
gat gtt gct gtt ttg cca ttt tcc aac agc aca aat aac ggg tta ttg 192  
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu  
50 55 60  
  
ttt ata aat act act att gcc agc att gct gct aaa gaa gaa ggg gta 240  
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val  
65 70 75 80  
  
tct ctc gag aaa aga gag gct gaa gct gaa ttc aaa gac aac gtt gcg 288  
Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala  
85 90 95  
  
gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc 336  
Asp Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg  
100 105 110  
  
aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat 384  
Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp  
115 120 125  
  
cgt gta ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg 432  
Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr  
130 135 140  
  
act atc aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc 480  
Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser  
145 150 155 160  
  
gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag 528  
Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln  
165 170 175  
  
agg acg act gga aat tca atc cat caa gca caa gac ggt aca acc act 576  
Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr  
180 185 190  
  
aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca 624  
Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala  
195 200 205  
  
ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc 672  
Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser

210	215	220	
ctt caa gac ctc aag gcg agc cct cag gcg aag cg <sup>g</sup> ctc gac agt gtg Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val			720
225	230	235	240
agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu			768
245	250		255
ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His			816
260	265		270
gag atc agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly			864
275	280		285
ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga Leu Ser Asn Ile Phe Ser Asp Lys Asp Gly Gly Gln Tyr Met Arg			912
290	295		300
tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu			960
305	310		315
gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln			1008
325	330		335
tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg			1056
340	345		350
agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg Ser Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu			1104
355	360		365
aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn			1152
370	375		380
tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro			1200
385	390		395
tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp			1248
405	410		415
ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp			1296
420	425		430
tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln			1344
435	440		445
cag tcc aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca			1392

Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala			
450	455	460	
gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc			1440
Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu			
465	470	475	480
gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc			1488
Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala			
485	490	495	
gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg			1536
Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr			
500	505	510	
ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg			1584
Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp			
515	520	525	
aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca			1632
Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala			
530	535	540	
gaa gtt gtg gct agc ctg gtg cca gca gca taggcggccg c			1673
Glu Val Val Ala Ser Leu Val Pro Ala Ala			
545	550		
<210> 17			
<211> 554			
<212> PRT			
<213> Exophiala spinifera			
<400> 17			
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser			
1	5	10	15
Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln			
20	25	30	
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe			
35	40	45	
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu			
50	55	60	
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val			
65	70	75	80
Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala			
85	90	95	

Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg  
100 105 110

Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp  
115 120 125

Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr  
130 135 140

Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser  
145 150 155 160

Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln  
165 170 175

Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr  
180 185 190

Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala  
195 200 205

Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser  
210 215 220

Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val  
225 230 235 240

Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu  
245 250 255

Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His  
260 265 270

Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly  
275 280 285

Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg  
290 295 300

Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu  
305 310 315 320

Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln  
325 330 335

Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg  
340 345 350

Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu  
355 360 365

Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn  
370 375 380

Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro  
385 390 395 400

Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp  
405 410 415

Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp  
420 425 430

Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln  
435 440 445

Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala  
450 455 460

Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu  
465 470 475 480

Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala  
485 490 495

Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr  
500 505 510

Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp  
515 520 525

Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala  
530 535 540

Glu Val Val Ala Ser Leu Val Pro Ala Ala  
545 550

<210> 18  
<211> 2079

<212> DNA  
 <213> Unknown

<220>  
 <223> GST:K:trAPAO 2079 for bacterial expression

<220>  
 <221> CDS  
 <222> (1)..(2076)  
 <223>

<220>  
 <221> misc\_feature  
 <222> (1)..(687)  
 <223> gst fusion + polylinker

<220>  
 <221> misc\_feature  
 <222> (688)..(2076)  
 <223> K:trAPAO

<220>  
 <221> misc\_feature  
 <222> (688)..(690)  
 <223> Extra lysine

<400> 18		
atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc		48
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro		
1 5 10 15		
act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg		96
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu		
20 25 30		
tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg		144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu		
35 40 45		
ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa		192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys		
50 55 60		
tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac		240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn		
65 70 75 80		
atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa		288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu		
85 90 95		
gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt		336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser		
100 105 110		
aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa		384

Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	
115					120							125				
atg	ctg	aaa	atg	ttc	gaa	gat	cgt	tta	tgt	cat	aaa	aca	tat	tta	aat	432
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	
130				135					140							
ggg	gat	cat	gta	acc	cat	cct	gac	ttc	atg	ttg	tat	gac	gct	ctt	gat	480
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	
145				150					155				160			
gtt	gtt	tta	tac	atg	gac	cca	atg	tgc	gtt	gct	ttc	cca	aaa	tta		528
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu	
				165				170				175				
gtt	tgt	ttt	aaa	aaa	cgt	att	gaa	gct	atc	cca	caa	att	gat	aag	tac	576
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr	
	180				185			185			190					
ttt	aaa	tcc	agc	aag	tat	ata	gca	tgg	cct	ttg	cag	ggc	tgg	caa	gcc	624
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala	
	195				200			200			205					
acg	ttt	ggg	ggg	gac	cat	cct	cca	aaa	tcg	gat	ctg	gtt	ccg	cgt		672
Thr	Phe	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg		
	210			215			215			220						
gga	tcc	ccg	gaa	ttc	aaa	gac	aac	gtt	gct	gac	gtt	gtt	gtt	gtt	ggc	720
Gly	Ser	Pro	Glu	Phe	Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	
	225			230			230			235			240			
gct	ggc	ttt	agg	ttt	gag	acg	gca	cgc	aaa	gtc	cag	gcc	gcc	ggg		768
Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	
	245			250			250			255			255			
ctg	tcc	tgc	ctc	gtt	ctt	gag	gct	atg	gat	cgt	gta	ggg	gga	aag	act	816
Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	
	260			265			265			270						
ctg	agc	gta	caa	tcg	ggg	ccc	ggc	agg	acg	act	atc	aac	gac	ctc	ggc	864
Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	
	275			280			280			285			285			
gct	ggc	tgg	atc	aat	gac	agg	aac	caa	agg	gaa	gta	tcc	aga	ttt		912
Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	
	290			295			295			300						
gaa	aga	ttt	cat	ttt	gag	ggc	gag	ctc	cag	agg	acg	act	gga	aat	tca	960
Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	
	305			310			310			315			320			
atc	cat	caa	gca	caa	gac	ggt	aca	acc	act	aca	gct	cct	tat	ggt	gac	1008
Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp		
	325			325			330			335						
tcc	ttt	ctg	agg	gag	ggg	gtt	gca	agt	gca	ctt	gct	gaa	ctc	ctc	ccc	1056
Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	
	340			345			345			350			350			

gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag gcg Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala	355	360	365	1104
agc cct cag gcg aag cg <sup>g</sup> ctc gac agt gtg agc ttc gcg cac tac tgt Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Phe Ala His Tyr Cys	370	375	380	1152
gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca aac cag atc Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile	385	390	395	400
aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc atg ctt ttt Thr Arg Ala Leu Leu Gly Val Ala His Glu Ile Ser Met Leu Phe	405	410	415	1248
ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat att ttc tcg Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser	420	425	430	1296
gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca ggt atg cag Asp Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln	435	440	445	1344
tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg cac Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His	450	455	460	1392
ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc ggc tgt aca Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr	465	470	475	480
gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val	485	490	495	1488
tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct ctt Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu	500	505	510	1536
ccc gcc gag aagcaa gca ttg gcg gaa aat tct atc ctg ggc tac tat Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr	515	520	525	1584
agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa ggc Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Arg Glu Gln Gly	530	535	540	1632
ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca ttt gcc aga Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg	545	550	555	1680
gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc atg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met	565	570	575	1728
gtc gga gac ccg gga cg <sup>g</sup> aag tgg tcc caa cag tcc aag cag gta cga Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg	580	585	590	1776

caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc ggg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly	595	600	605	1824
gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tcg aag Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys	610	615	620	1872
cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ctg aac gat Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp	625	630	635	1920
ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag agt gtt cat Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His	645	650	655	1968
ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa ggg Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly	660	665	670	2016
gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg gct agc ctg Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu	675	680	685	2064
gtg cca gca gca tag Val Pro Ala Ala				2079
	690			

<210> 19  
<211> 692  
<212> PRT  
<213> Unknown

<220>  
<223> GST:K:trAPAO 2079 for bacterial expression

<220>  
<221> misc\_feature  
<222> (1)..(687)  
<223> gst fusion + polylinker

<220>  
<221> misc\_feature  
<222> (688)..(2076)  
<223> K:trAPAO

<220>  
<221> misc\_feature  
<222> (688)..(690)  
<223> Extra lysine

<400> 19

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
1 5 10 15

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
20 25 30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
65 70 75 80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
85 90 95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
100 105 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
115 120 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
130 135 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
180 185 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
195 200 205

Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
210 215 220

Gly Ser Pro Glu Phe Lys Asp Asn Val Ala Asp Val Val Val Gly  
225 230 235 240

Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly  
245 250 255

Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr  
260 265 270

Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly  
275 280 285

Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe  
290 295 300

Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser  
305 310 315 320

Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp  
325 330 335

Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro  
340 345 350

Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala  
355 360 365

Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys  
370 375 380

Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile  
385 390 395 400

Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe  
405 410 415

Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser  
420 425 430

Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln  
435 440 445

Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His  
450 455 460

Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr  
465 470 475 480

Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val  
485 490 495

Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu  
500 505 510

Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr  
515 520 525

Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly  
530 535 540

Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg  
545 550 555 560

Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met  
565 570 575

Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg  
580 585 590

Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly  
595 600 605

Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys  
610 615 620

Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp  
625 630 635 640

Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His  
645 650 655

Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly  
660 665 670

Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu  
675 680 685

Val Pro Ala Ala  
690

<210> 20  
<211> 1464  
<212> DNA  
<213> Unknown

<220>  
<223> K:trAPAO translational fusion with barley alpha amylase

<220>  
<221> sig\_peptide  
<222> (1)..(72)  
<223> Barley alpha amylase signal sequence

<220>  
<221> misc\_feature  
<222> (73)..(1464)  
<223> K:trAPAO cDNA

<220>  
<221> CDS  
<222> (1)..(1461)  
<223>

<220>  
<221> misc\_feature  
<222> (73)..(75)  
<223> Added lysine residue

<400> 20		
atg gcc aac aag cac ctg agc ctc tcc ctc ttc ctc gtg ctc ctc ggc		48
Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly		
1	5	10
		15
ctc tcc gcc tcc ctc gcc agc ggc aaa gac aac gtt gcg gac gtg gta		96
Leu Ser Ala Ser Leu Ala Ser Gly Lys Asp Asn Val Ala Asp Val Val		
20	25	30
gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag		144
Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln		
35	40	45
gcc gcc ggt ctg tcc ctc gtt ctt gag gcg atg gat cgt gta ggg		192
Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly		
50	55	60
gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac		240
Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn		
65	70	75
80		
gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc		288
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser		
85	90	95
aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act		336
Arg Leu Phe Glu Arg Phe His Leu Glu Gly Leu Gln Arg Thr Thr		
100	105	110
gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct cct		384
Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro		
115	120	125

tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa		432
Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu		
130	135	140
ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac		480
Leu Leu Pro Val Trp Ser Gln Leu Ile Glu His Ser Leu Gln Asp		
145	150	155
160		
ctc aag gcg agc cct cag gcg aag cg <sup>g</sup> ctc gac agt gtg agc ttc gcg		528
Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala		
165	170	175
cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca		576
His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala		
180	185	190
aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc		624
Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser		
195	200	205
atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat		672
Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn		
210	215	220
att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca		720
Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr		
225	230	235
240		
ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc		768
Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly		
245	250	255
tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc		816
Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser		
260	265	270
ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag		864
Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys		
275	280	285
gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca		912
Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser		
290	295	300
cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg		960
Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu		
305	310	315
320		
ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc		1008
Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg		
325	330	335
gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca		1056
Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser		
340	345	350
ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att acc		1104
Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr		
355	360	365

tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag		1152	
Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys			
370	375	380	
cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag		1200	
Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu			
385	390	395	400
aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag		1248	
Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu			
405	410	415	
tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg		1296	
Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly			
420	425	430	
ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag		1344	
Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys			
435	440	445	
agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat		1392	
Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr			
450	455	460	
atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg		1440	
Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val			
465	470	475	480
gct agc ctg gtg cca gca gca tag		1464	
Ala Ser Leu Val Pro Ala Ala			
485			

<210> 21  
<211> 487  
<212> PRT  
<213> Unknown

<220>  
<223> K:trAPAO translational fusion with barley alpha amylase

<220>  
<221> misc\_feature  
<222> (73)..(1464)  
<223> K:trAPAO cDNA

<220>  
<221> misc\_feature  
<222> (73)..(75)  
<223> Added lysine residue

<400> 21

Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly  
1 5 10 15

Leu Ser Ala Ser Leu Ala Ser Gly Lys Asp Asn Val Ala Asp Val Val

20

25

30

Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln  
35 40 45

Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly  
50 55 60

Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn  
65 70 75 80

Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser  
85 90 95

Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr  
100 105 110

Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro  
115 120 125

Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu  
130 135 140

Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp  
145 150 155 160

Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala  
165 170 175

His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala  
180 185 190

Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser  
195 200 205

Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn  
210 215 220

Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr  
225 230 235 240

Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly  
245 250 255

Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser  
260 265 270

Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys  
275 280 285

Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser  
290 295 300

Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu  
305 310 315 320

Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg  
325 330 335

Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser  
340 345 350

Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr  
355 360 365

Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys  
370 375 380

Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu  
385 390 395 400

Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu  
405 410 415

Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly  
420 425 430

Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys  
435 440 445

Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr  
450 455 460

Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val  
465 470 475 480

Ala Ser Leu Val Pro Ala Ala  
485

<210>	22		
<211>	1803		
<212>	DNA		
<213>	Exophiala spinifera		
<220>			
<221>	CDS		
<222>	(1)...(1800)		
<223>			
<400>	22		
atg gca ctt gca ccg agc tac atc aat ccc cca aac gtc gcc tcc cca			48
Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro			
1	5	10	15
gca ggg tat tct cac gtc ggc gta ggc cca gac gga ggg agg tat gtg			96
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val			
20	25	30	
aca ata gct gga cag att gga caa gac gct tcg ggc gtg aca gac cct			144
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro			
35	40	45	
gcc tac gag aaa cag gtt gcc caa gca ttc gcc aat ctg cga gct tgc			192
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys			
50	55	60	
ctt gct gca gtt gga gcc act tca aac gac gtc acc aag ctc aat tac			240
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr			
65	70	75	80
tac atc gtc gac tac gcc ccg agc aaa ctc acc gca att gga gat ggg			288
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly			
85	90	95	
ctg aag gct acc ttt gcc ctt gac agg ctc cct cct tgc acg ctg gtg			336
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val			
100	105	110	
cca gtg tcg gcc ttg tct tca cct gaa tac ctc ttt gag gtt gat gcc			384
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala			
115	120	125	
acg gcg ctg gtg ccg gga cac acg acc cca gac aac gtt gcg gac gtg			432
Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val			
130	135	140	
gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc			480
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val			
145	150	155	160
cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta			528
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val			
165	170	175	
ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc			576
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile			
180	185	190	

aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val 195 200 205	624
tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr 210 215 220	672
act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala 225 230 235 240	720
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt qcg Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala 245 250 255	768
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln 260 265 270	816
gac ctc aag gcg agc cct cag gcg aag cggt ctc gac agt gtg agc ttc Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe 275 280 285	864
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val 290 295 300	912
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile 305 310 315 320	960
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser 325 330 335	1008
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys 340 345 350	1056
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro 355 360 365	1104
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala 370 375 380	1152
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys 385 390 395 400	1200
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe 405 410 415	1248
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile	1296

420

425

430

ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg 1344  
 Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp  
 435 440 445

cgc gaa caa ggc ttc tcg ggc ctc caa tcg agc tgt gac ccc atc 1392  
 Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile  
 450 455 460

tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att 1440  
 Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile  
 465 470 475 480

acc tgt ttc atg gtc gga gac ccg gga cgaa ggg tgg tcc caa cag tcc 1488  
 Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser  
 485 490 495

aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac 1536  
 Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr  
 500 505 510

gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc 1584  
 Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile  
 515 520 525

gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat 1632  
 Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr  
 530 535 540

ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc 1680  
 Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe  
 545 550 555 560

aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg 1728  
 Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly  
 565 570 575

tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt 1776  
 Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val  
 580 585 590

gtg gct agc ctg gtg cca gca gca tag 1803  
 Val Ala Ser Leu Val Pro Ala Ala  
 595 600

<210> 23  
 <211> 600  
 <212> PRT  
 <213> Exophiala spinifera

<400> 23

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro  
 1 5 10 15

Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val

20

25

30

Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro  
35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys  
50 55 60

Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr  
65 70 75 80

Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly  
85 90 95

Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val  
100 105 110

Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala  
115 120 125

Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val  
130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val  
145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val  
165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile  
180 185 190

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val  
195 200 205

Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr  
210 215 220

Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala  
225 230 235 240

Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala  
245 250 255

Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln  
260 265 270

Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe  
275 280 285

Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val  
290 295 300

Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile  
305 310 315 320

Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser  
325 330 335

Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys  
340 345 350

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro  
355 360 365

Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala  
370 375 380

Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys  
385 390 395 400

Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe  
405 410 415

Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile  
420 425 430

Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp  
435 440 445

Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile  
450 455 460

Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile  
465 470 475 480

Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser  
485 490 495

Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr  
500 505 510

Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile  
515 520 525

Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr  
530 535 540

Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe  
545 550 555 560

Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly  
565 570 575

Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val  
580 585 590

Val Ala Ser Leu Val Pro Ala Ala  
595 600

<210> 24  
<211> 3003  
<212> DNA  
<213> unknown

<220>  
<223> K:trAPAO

<220>  
<221> misc\_feature  
<222> (73)..(1575)  
<223> espl mat

<220>  
<221> misc\_feature  
<222> (1576)..(1611)  
<223> spacer sequence

<220>  
<221> misc\_feature  
<222> (1612)..(3000)  
<223> K:trAPAO

<220>  
<221> CDS  
<222> (1)..(3000)  
<223>

```
<220>
<221> misc_feature
<222> (1612)..(1614)
<223> extra lysine
```

<400> 24  
 atg gcc aac aag cac ctg agc ctc tcc ctc ttc ctc gtg ctc ctc ggc 48  
 Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly  
 1 5 10 15  
  
 ctc tcc gcc tcc ctc gcc agc ggc gct cct act gtc aag att gat gct 96  
 Leu Ser Ala Ser Leu Ala Ser Gly Ala Pro Thr Val Lys Ile Asp Ala  
 20 25 30  
  
 ggg atg gtg gtc ggc acg act act act gtc ccc ggc acc act gcg acc 144  
 Gly Met Val Val Gly Thr Thr Thr Val Pro Gly Thr Thr Ala Thr  
 35 40 45  
  
 gtc agc gag ttc ttg ggc gtt cct ttt gcc gcc tct ccg aca cga ttt 192  
 Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe  
 50 55 60  
  
 gcg cct cct act cgt ccc gtg cct tgg tca acg cct ttg caa gcc act 240  
 Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr  
 65 70 75 80  
  
 gca tat ggt cca gca tgc cct caa caa ttc aat tac ccc gaa gaa ctc 288  
 Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu  
 85 90 95  
  
 cgt gag att acg atg gcc tgg ttc aat aca ccg ccc ccg tca gct ggt 336  
 Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly  
 100 105 110  
  
 gaa agt gag gac tgc ctg aac ctc aac atc tac gtc cca gga act gag 384  
 Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu  
 115 120 125  
  
 aac aca aac aaa gcc gtc atg gtt tgg ata tac ggt gga gcg ctg gaa 432  
 Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Ala Leu Glu  
 130 135 140  
  
 tat ggt tgg aat tca ttc cac ctt tac gac ggg gct agt ttc gca gcc 480  
 Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala  
 145 150 155 160  
  
 aat cag gat gtc atc gcc gtg acc atc aac tac aga acg aac att ctg 528  
 Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu  
 165 170 175  
  
 ggg ttc cct gct gcc cct cag ctt cca ata aca cag cga aat ctg ggg 576  
 Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly  
 180 185 190  
  
 ttc cta gac caa agg ttt gct ttg gat tgg gta cag cgg aac atc gca 624  
 Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala  
 195 200 205

gcc ttt ggc ggt gat cct cga aag gtc aca ata ttt ggg cag agt gcg Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala 210 215 220	672
ggg ggc aga agt gtc gac gtc ctc ttg acg tct atg cca cac aac cca Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro 225 230 235 240	720
ccc ttc cga gca gca atc atg gag tcc ggt gtg gct aac tac aac ttc Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe 245 250 255	768
ccc aag gga gat ttg tcc gaa cct tgg aac acc act gtt caa gct ctc Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu 260 265 270	816
aac tgt acc acc agt atc gac atc ttg agt tgt atg aga aga gtc gat Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp 275 280 285	864
ctc gcc act ctg atg aac acg atc gag caa ctc gga ctt ggg ttt gag Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu 290 295 300	912
tac acg ttg gac aac gta acg gct gtg tac cgt tct gaa acg gct cgc Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg 305 310 315 320	960
acg act ggt gac att gct cgt gta cct gtt ctc gtc ggg acg gtg gcc Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala 325 330 335	1008
aac gac gga ctt ctc ttt gtc ctc ggg gag aat gac acc caa gca tat Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr 340 345 350	1056
ctc gag gag gca atc ccg aat cag ccc gac ctt tac cag act ctc ctt Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu 355 360 365	1104
gga gca tat ccc att gga tcc cca ggg atc gga tcg cct caa gat cag Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln 370 375 380	1152
att gcc gcc att gag acc gag gta aga ttc cag tgt cct tct gcc atc Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile 385 390 395 400	1200
gtg gct cag gac tcc cgg aat cgg ggt atc cct tct tgg cgc tac tac Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr 405 410 415	1248
tac aat gcg acc ttt gag aat ctg gag ctt ttc cct ggg tcc gaa gtg Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val 420 425 430	1296
tac cac agc tct gaa gtc ggg atg gtg ttt ggc acg tat cct gtc gca Tyr His Ser Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala	1344

435

440

445

agt gcg acc gcc ttg gag gcc cag acg agc aaa tac atg cag ggt gcc 1392  
 Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala  
   450                          455                          460  
  
 tgg gcg gcc ttt gcc aaa aac ccc atg aat ggg cct ggg tgg aaa caa 1440  
 Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln  
   465                          470                          475                          480  
  
 gtg ccg aat gtc gcg gcg ctt ggc tca cca ggc aaa gcc atc cag gtt 1488  
 Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val  
   485                          490                          495  
  
 gac gtc tct cca gcg aca ata gac caa cga tgt gcc ttg tac acg cgt 1536  
 Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg  
   500                          505                          510  
  
 tat tat act gag ttg ggc aca atc gcg ccg agg aca ttt ggc gga ggc 1584  
 Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly  
   515                          520                          525  
  
 agc ggc gga ggc agc ggc gga ggc agc aaa gac aac gtt gcg gac gtc 1632  
 Ser Gly Gly Ser Gly Gly Ser Lys Asp Asn Val Ala Asp Val  
   530                          535                          540  
  
 gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc 1680  
 Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val  
   545                          550                          555                          560  
  
 cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta 1728  
 Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val  
   565                          570                          575  
  
 ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc 1776  
 Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile  
   580                          585                          590  
  
 aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta 1824  
 Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val  
   595                          600                          605  
  
 tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg 1872  
 Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr  
   610                          615                          620  
  
 act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct 1920  
 Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala  
   625                          630                          635                          640  
  
 cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg 1968  
 Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala  
   645                          650                          655  
  
 gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa 2016  
 Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln  
   660                          665                          670  
  
 gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc 2064

Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe			
675	680	685	
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val			2112
690	695	700	
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile			2160
705	710	715	720
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser			2208
725	730	735	
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa Asn Ile Phe Ser Asp Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys			2256
740	745	750	
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro			2304
755	760	765	
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala			2352
770	775	780	
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys			2400
785	790	795	800
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe			2448
805	810	815	
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile			2496
820	825	830	
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp			2544
835	840	845	
cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile			2592
850	855	860	
tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile			2640
865	870	875	880
acc tgt ttc atg gtc gga gac ccg gga aag tgg tcc caa cag tcc Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser			2688
885	890	895	
aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr			2736
900	905	910	

gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc		2784
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile		
915	920	925
gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat		2832
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr		
930	935	940
ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc		2880
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe		
945	950	955
aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg		2928
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly		
965	970	975
tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt		2976
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val		
980	985	990
gtg gct agc ctg gtg cca gca gca tag		3003
Val Ala Ser Leu Val Pro Ala Ala		
995	1000	

<210> 25  
<211> 1000  
<212> PRT  
<213> unknown

<220>  
<223> K:trAPAO

<220>  
<221> misc\_feature  
<222> (73)..(1575)  
<223> espl mat

<220>  
<221> misc\_feature  
<222> (1576)..(1611)  
<223> spacer sequence

<220>  
<221> misc\_feature  
<222> (1612)..(3000)  
<223> K:trAPAO

<220>  
<221> misc\_feature  
<222> (1612)..(1614)  
<223> extra lysine

<400> 25

Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly		
1	5	10
		15

Leu Ser Ala Ser Leu Ala Ser Gly Ala Pro Thr Val Lys Ile Asp Ala  
20 25 30

Gly Met Val Val Gly Thr Thr Thr Thr Val Pro Gly Thr Thr Ala Thr  
35 40 45

Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe  
50 55 60

Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr  
65 70 75 80

Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu  
85 90 95

Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly  
100 105 110

Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu  
115 120 125

Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu  
130 135 140

Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala  
145 150 155 160

Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu  
165 170 175

Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly  
180 185 190

Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala  
195 200 205

Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala  
210 215 220

Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro  
225 230 235 240

Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe  
245 250 255

Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu  
260 265 270

Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp  
275 280 285

Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu  
290 295 300

Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg  
305 310 315 320

Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala  
325 330 335

Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr  
340 345 350

Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu  
355 360 365

Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln  
370 375 380

Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile  
385 390 395 400

Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr  
405 410 415

Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val  
420 425 430

Tyr His Ser Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala  
435 440 445

Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala  
450 455 460

Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln  
465 470 475 480

Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val  
485 490 495

Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg  
500 505 510

Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly  
515 520 525

Ser Gly Gly Ser Gly Gly Ser Lys Asp Asn Val Ala Asp Val  
530 535 540

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val  
545 550 555 560

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val  
565 570 575

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile  
580 585 590

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val  
595 600 605

Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr  
610 615 620

Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala  
625 630 635 640

Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala  
645 650 655

Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln  
660 665 670

Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe  
675 680 685

Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val  
690 695 700

Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile  
705 710 715 720

Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser

725

730

735

Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys  
740 745 750

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro  
755 760 765

Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala  
770 775 780

Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys  
785 790 795 800

Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe  
805 810 815

Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile  
820 825 830

Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp  
835 840 845

Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile  
850 855 860

Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile  
865 870 875 880

Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser  
885 890 895

Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr  
900 905 910

Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile  
915 920 925

Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr  
930 935 940

Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe  
945 950 955 960

Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly  
965 970 975

Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val  
980 985 990

Val Ala Ser Leu Val Pro Ala Ala  
995 1000

<210> 26  
<211> 2976  
<212> DNA  
<213> Unknown

<220>  
<223> Barley alpha amylase signal sequence:BEST1 mature:artificial spacer:K:trAPAO

<220>  
<221> sig\_peptide  
<222> (1)..(72)  
<223> Barley alpha amylase signal sequence

<220>  
<221> mat\_peptide  
<222> (73)..(1545)  
<223> BEST1 mature

<220>  
<221> misc\_feature  
<222> (1546)..(1584)  
<223> spacer sequence

<220>  
<221> misc\_feature  
<222> (1585)..(2973)  
<223> K:trAPAO

<220>  
<221> CDS  
<222> (1)..(2973)  
<223>

<220>  
<221> misc\_feature  
<222> (1585)..(1587)  
<223> Extra lysine

<400> 26  
atg gcc aac aag cac ctg agc ctc tcc ctc ttc ctc gtg ctc ctc ggc  
Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly

-20

-15

-10

ctc tcc gcc tcc ctc gcc agc ggc acg gat ttt ccg gtc cgc agg acc Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr -5 -1 1 5	96
gat ctg ggc cag gtt cag gga ctg gcc ggg gac gtg atg agc ttt cgc Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg 10 15 20	144
gga ata ccc tat gca gcg ccg gtg ggc ggg ctg cgt tgg aag ccg Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro 25 30 35 40	192
ccc caa cac gcc cgg ccc tgg gcg ggc gtt cgc ccc gcc acc caa ttt Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe 45 50 55	240
ggc tcc gac tgc ttc ggc gcg gcc tat ctt cgc aaa ggc agc ctc gcc Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala 60 65 70	288
ccc ggc gtg agc gag gac tgt ctt tac ctc aac gta tgg gcg ccg tca Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser 75 80 85	336
ggc gct aaa ccc ggc cag tac ccc gtc atg gtc tgg gtc tac ggc ggc Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly 90 95 100	384
ggc ttc gcc ggc acg gcc gcc atg ccc tac tac gac ggc gag gcg Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala 105 110 115 120	432
ctt gcg cga cag ggc gtc gtg gtg acg ttt aac tat cgg acg aac Leu Ala Arg Gln Gly Val Val Val Thr Phe Asn Tyr Arg Thr Asn 125 130 135	480
atc ctg ggc ttt ttc gcc cat cct ggt ctc tcg cgc gag agc ccc acc Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr 140 145 150	528
gga act tcg ggc aac tac ggc cta ctc gac att ctc gcc gct ctt cgg Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg 155 160 165	576
tgg gtg cag agc aac gcc cgc gcc ttc gga ggg gac ccc ggc cga gtg Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val 170 175 180	624
acg gtc ttt ggt gaa tcg gcc gga gcg agc gcg atc gga ctt ctg ctc Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu 185 190 195 200	672
acc tcg ccg ctg agc aag ggt ctc ttc cgt ggc gct atc ctc gaa agt Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser 205 210 215	720
cca ggg ctg acg cga ccg ctc gcg acg ctc gcc gac agc gcc gcc tcg	768

Pro	Gly	Leu	Thr	Arg	Pro	Leu	Ala	Thr	Leu	Ala	Asp	Ser	Ala	Ala	Ser	
220					225							230				
ggc gag cgc ctc gac gcc gat ctt tcg cga ctg cgc tcg acc gac cca															816	
Gly	Glu	Arg	Leu	Asp	Ala	Asp	Leu	Ser	Arg	Leu	Arg	Ser	Thr	Asp	Pro	
235					240							245				
gcc acc ctg atg gcg cgc gcc gac gcg gcc cgc ccg gca tcg cgg gac															864	
Ala	Thr	Leu	Met	Ala	Arg	Ala	Asp	Ala	Ala	Arg	Pro	Ala	Ser	Arg	Asp	
250					255							260				
ctg cgc agg ccg cgt ccg acc gga ccg atc gtc gat ggc cat gtg ctg															912	
Leu	Arg	Arg	Pro	Arg	Pro	Thr	Gly	Pro	Ile	Val	Asp	Gly	His	Val	Leu	
265					270							275			280	
ccg cag acc gac agc gcg gcg atc gcg gcg ggg cag ctg gcg ccg gtt															960	
Pro	Gln	Thr	Asp	Ser	Ala	Ala	Ile	Ala	Ala	Gly	Gln	Leu	Ala	Pro	Val	
285					290							295				
cgg gtc ctg atc gga acc aat gcc gac gaa ggc cgc gcc ttc ctc ggg															1008	
Arg	Val	Leu	Ile	Gly	Thr	Asn	Ala	Asp	Glu	Gly	Arg	Ala	Phe	Leu	Gly	
300					305							310				
cgc gcg ccg atg gag acg cca gcg gac tac caa gcc tat ctg gag gcg															1056	
Arg	Ala	Pro	Met	Glu	Thr	Pro	Ala	Asp	Tyr	Gln	Ala	Tyr	Leu	Glu	Ala	
315					320							325				
cag ttt ggc gac caa gcc gcc gtg gcg gcg tgc tat ccc ctc gac															1104	
Gln	Phe	Gly	Asp	Gln	Ala	Ala	Val	Ala	Ala	Cys	Tyr	Pro	Leu	Asp		
330					335							340				
ggc cgg gcc acg ccc aag gaa atg gtc gcg cgc atc ttc ggc gac aat															1152	
Gly	Arg	Ala	Thr	Pro	Lys	Glu	Met	Val	Ala	Arg	Ile	Phe	Gly	Asp	Asn	
345					350							355			360	
cag ttc aat cgg ggg gtc tcg gcc ttc tcg gaa gcg ctt gtg cgc cag															1200	
Gln	Phe	Asn	Arg	Gly	Val	Ser	Ala	Phe	Ser	Glu	Ala	Leu	Val	Arg	Gln	
365					370							375				
ggc gcg ccc gtg tgg cgt tat cag ttc aac ggt aat acc gag ggt gga															1248	
Gly	Ala	Pro	Val	Trp	Arg	Tyr	Gln	Phe	Asn	Gly	Asn	Thr	Glu	Gly	Gly	
380					385							390				
aga gcg ccg gct acc cac gga gcc gaa att ccc tac gtt ttc ggg gtg															1296	
Arg	Ala	Pro	Ala	Thr	His	Gly	Ala	Glu	Ile	Pro	Tyr	Val	Phe	Gly	Val	
395					400							405				
ttc aag ctc gac gag ttg ggt ctg ttc gat tgg ccg ccc gag ggg ccc															1344	
Phe	Lys	Leu	Asp	Glu	Leu	Gly	Leu	Phe	Asp	Trp	Pro	Pro	Glu	Gly	Pro	
410					415							420				
acg ccc gcc gac cgt gcg ctg ggc caa ctg atg tcc tcc gcc tgg gtc															1392	
Thr	Pro	Ala	Asp	Arg	Ala	Leu	Gly	Gln	Leu	Met	Ser	Ser	Ala	Trp	Val	
425					430							435			440	
cgg ttc gcc aag aat ggc gac ccc gcc ggg gac gcc ctt acc tgg cct															1440	
Arg	Phe	Ala	Lys	Asn	Gly	Asp	Pro	Ala	Gly	Asp	Ala	Leu	Thr	Trp	Pro	
445					450							455				

gcc tat tct acg ggc aag tcg acc atg aca ttc ggt ccc gag ggc cgc Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg	460	465	470	1488	
gcg gcg gtg gtg tcg ccc gga cct tcc atc ccc cct tgc gcg gat ggc Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly	475	480	485	1536	
gcc aag gcg ggg ggc gga ggc agc ggc gga ggc agc ggc gga ggc agc Ala Lys Ala Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Ser	490	495	500	1584	
aaa gac aac gtt gcg gac gtg gta gtg gtc gct ggc ttg agc ggt Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly	505	510	515	520	1632
ttg gag acg gca cgc aaa gtc cag gcc ggc ggt ctg tcc tgc ctc gtt Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val	525	530	535		1680
ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser	540	545	550		1728
ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn	555	560	565		1776
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu	570	575	580		1824
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln	585	590	595	600	1872
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag Asp Gly Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu	605	610	615		1920
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu	620	625	630		1968
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys	635	640	645		2016
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn	650	655	660		2064
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu	665	670	675	680	2112
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	685	690	695		2160

aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly 700 705 710	2208
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala 715 720 725	2256
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val 730 735 740	2304
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser 745 750 755 760	2352
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc Gly Ala Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr 765 770 775	2400
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln 780 785 790	2448
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe 795 800 805	2496
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu 810 815 820	2544
caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp 825 830 835 840	2592
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly 845 850 855	2640
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp 860 865 870	2688
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu 875 880 885	2736
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln 890 895 900	2784
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly 905 910 915 920	2832
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu	2880

925

930

935

acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt  
 Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly  
 940 945 950

2928

caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag  
 Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
 955 960 965

2976

<210> 27  
 <211> 991  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Barley alpha amylase signal sequence:BEST1 mature:artificial spacer:K:trAPAO

<220>  
 <221> misc\_feature  
 <222> (1546)..(1584)  
 <223> spacer sequence

<220>  
 <221> misc\_feature  
 <222> (1585)..(2973)  
 <223> K:trAPAO

<220>  
 <221> misc\_feature  
 <222> (1585)..(1587)  
 <223> Extra lysine

<400> 27

Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly  
 -20 -15 -10

Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr  
 -5 -1 1 5

Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg  
 10 15 20

Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro  
 25 30 35 40

Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe  
 45 50 55

Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala  
 60 65 70

Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser  
75 80 85

Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly  
90 95 100

Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala  
105 110 115 120

Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn  
125 130 135

Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr  
140 145 150

Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg  
155 160 165

Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val  
170 175 180

Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu  
185 190 195 200

Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser  
205 210 215

Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser  
220 225 230

Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro  
235 240 245

Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp  
250 255 260

Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu  
265 270 275 280

Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val  
285 290 295

Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly

300

305

310

Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala  
315 320 325

Gln Phe Gly Asp Gln Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp  
330 335 340

Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn  
345 350 355 360

Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln  
365 370 375

Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly  
380 385 390

Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val  
395 400 405

Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro  
410 415 420

Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val  
425 430 435 440

Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro  
445 450 455

Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg  
460 465 470

Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly  
475 480 485

Ala Lys Ala Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser  
490 495 500

Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly  
505 510 515 520

Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val  
525 530 535

Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser  
540 545 550

Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn  
555 560 565

Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu  
570 575 580

Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln  
585 590 595 600

Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu  
605 610 615

Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu  
620 625 630

Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys  
635 640 645

Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn  
650 655 660

Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu  
665 670 675 680

Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile  
685 690 695

Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly  
700 705 710

Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala  
715 720 725

Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val  
730 735 740

Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser  
745 750 755 760

Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr  
765 770 775

Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln  
780 785 790

Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe  
795 800 805

Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu  
810 815 820

Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp  
825 830 835 840

Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly  
845 850 855

Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp  
860 865 870

Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu  
875 880 885

Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln  
890 895 900

Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly  
905 910 915 920

Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu  
925 930 935

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly  
940 945 950

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
955 960 965

<210> 28  
<211> 3618  
<212> DNA  
<213> Unknown

<220>  
<223> gst:espl:sp:K:trAPAO

<220>  
<221> CDS

<222> (1)..(3615)  
 <223>  
  
 <220>  
 <221> misc\_feature  
 <222> (1)..(687)  
 <223> gst + polylinker  
  
 <220>  
 <221> mat\_peptide  
 <222> (688)..(2190)  
 <223> esp1 mat  
  
 <220>  
 <221> misc\_feature  
 <222> (2191)..(2226)  
 <223> spacer sequence  
  
 <220>  
 <221> misc\_feature  
 <222> (2227)..(3615)  
 <223> K:trAPAO  
  
 <220>  
 <221> misc\_feature  
 <222> (2227)..(2229)  
 <223> extra lysine  
  
 <400> 28
 

atg tcc cct ata cta	ggt tat tgg aaa att	aag ggc ctt gtg caa	45
Met Ser Pro Ile Leu	Gly Tyr Trp Lys Ile	Lys Gly Leu Val Gln	
-225	-220	-215	
ccc act cga ctt ctt	ttg gaa tat ctt gaa	gaa aaa tat gaa gag	90
Pro Thr Arg Leu Leu	Leu Glu Tyr Leu Glu	Glu Lys Tyr Glu Glu	
-210	-205	-200	
cat ttg tat gag cgc	gat gaa ggt gat aaa	tgg cga aac aaa aag	135
His Leu Tyr Glu Arg	Asp Glu Gly Asp Lys	Trp Arg Asn Lys Lys	
-195	-190	-185	
ttt gaa ttg ggt ttg	gag ttt ccc aat ctt	cct tat tat att gat	180
Phe Glu Leu Gly Leu	Glu Phe Pro Asn Leu	Pro Tyr Tyr Ile Asp	
-180	-175	-170	
ggt gat gtt aaa tta	aca cag tct atg gcc	atc ata cgt tat ata	225
Gly Asp Val Lys Leu	Thr Gln Ser Met Ala	Ile Ile Arg Tyr Ile	
-165	-160	-155	
gct gac aag cac aac	atg ttg ggt tgt	cca aaa gag cgt gca	270
Ala Asp Lys His Asn	Met Leu Gly Gly Cys	Pro Lys Glu Arg Ala	
-150	-145	-140	
gag att tca atg ctt	gaa gga gcg gtt ttg	gat att aga tac ggt	315

Glu Ile Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly			
-135	-130	-125	
gtt tcg aga att gca tat agt aaa gac ttt gaa act ctc aaa gtt			360
Val Ser Arg Ile Ala Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val			
-120	-115	-110	
gat ttt ctt agc aag cta cct gaa atg ctg aaa atg ttc gaa gat cgt			408
Asp Phe Leu Ser Lys Leu Pro Glu Met Leu Lys Met Phe Glu Asp Arg			
-105	-100	-95	
tta tgt cat aaa aca tat tta aat ggt gat cat gta acc cat cct gac			456
Leu Cys His Lys Thr Tyr Leu Asn Gly Asp His Val Thr His Pro Asp			
-90	-85	-80	
ttc atg ttg tat gac gct ctt gat gtt gtt tta tac atg gac cca atg			504
Phe Met Leu Tyr Asp Ala Leu Asp Val Val Leu Tyr Met Asp Pro Met			
-75	-70	-65	
tgc ctg gat gcg ttc cca aaa tta gtt tgt ttt aaa aaa cgt att gaa			552
Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys Lys Arg Ile Glu			
-60	-55	-50	
gct atc cca caa att gat aag tac ttg aaa tcc agc aag tat ata gca			600
Ala Ile Pro Gln Ile Asp Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala			
-45	-40	-35	-30
tgg cct ttg cag ggc tgg caa gcc acg ttt ggt ggc gac cat cct			648
Trp Pro Leu Gln Gly Trp Gln Ala Thr Phe Gly Gly Asp His Pro			
-25	-20	-15	
cca aaa tcg gat ctg gtt ccg cgt gga tcc ccg gaa ttc gct cct act			696
Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Glu Phe Ala Pro Thr			
-10	-5	-1	1
gtc aag att gat gct ggg atg gtg gtc ggc acg act act act gtc ccc			744
Val Lys Ile Asp Ala Gly Met Val Val Gly Thr Thr Thr Thr Val Pro			
5	10	15	
ggc acc act gcg acc gtc acg gag ttc ttg ggc gtt cct ttt gcc gcc			792
Gly Thr Thr Ala Thr Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala			
20	25	30	35
tct ccg aca cga ttt gcg cct cct act cgt ccc gtg cct tgg tca acg			840
Ser Pro Thr Arg Phe Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr			
40	45	50	
cct ttg caa gcc act gca tat ggt cca gca tgc cct caa caa ttc aat			888
Pro Leu Gln Ala Thr Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn			
55	60	65	
tac ccc gaa gaa ctc cgt gag att acg atg gcc tgg ttc aat aca ccg			936
Tyr Pro Glu Glu Leu Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro			
70	75	80	
ccc ccg tca gct ggt gaa agt gag gac tgc ctg aac ctc aac atc tac			984
Pro Pro Ser Ala Gly Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr			
85	90	95	

gtc cca gga act gag aac aca aac aaa gcc gtc atg gtt tgg ata tac		1032
Val Pro Gly Thr Glu Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr		
100	105	110
		115
ggt gga gcg ctg gaa tat ggt tgg aat tca ttc cac ctt tac gac ggg		1080
Gly Gly Ala Leu Glu Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly		
120	125	130
gct agt ttc gca gcc aat cag gat gtc atc gcc gtg acc atc aac tac		1128
Ala Ser Phe Ala Ala Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr		
135	140	145
aga acg aac att ctg ggg ttc cct gct gcc cct cag ctt cca ata aca		1176
Arg Thr Asn Ile Leu Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr		
150	155	160
cag cga aat ctg ggg ttc cta gac caa agg ttt gct ttg gat tgg gta		1224
Gln Arg Asn Leu Gly Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val		
165	170	175
cag cgg aac atc gca gcc ttt ggc ggt gat cct cga aag gtc aca ata		1272
Gln Arg Asn Ile Ala Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile		
180	185	190
		195
ttt ggg cag agt gcg ggg ggc aga agt gtc gac gtc ctc ttg acg tct		1320
Phe Gly Gln Ser Ala Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser		
200	205	210
atg cca cac aac cca ccc ttc cga gca gca atc atg gag tcc ggt gtg		1368
Met Pro His Asn Pro Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val		
215	220	225
gct aac tac aac ttc ccc aag gga gat ttg tcc gaa cct tgg aac acc		1416
Ala Asn Tyr Asn Phe Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr		
230	235	240
act gtt caa gct ctc aac tgt acc acc agt atc gac atc ttg agt tgt		1464
Thr Val Gln Ala Leu Asn Cys Thr Ser Ile Asp Ile Leu Ser Cys		
245	250	255
atg aga aga gtc gat ctc gcc act ctg atg aac acg atc gag caa ctc		1512
Met Arg Arg Val Asp Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu		
260	265	270
		275
gga ctt ggg ttt gag tac acg ttg gac aac gta acg gct gtg tac cgt		1560
Gly Leu Gly Phe Glu Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg		
280	285	290
tct gaa acg gct cgc acg act ggt gac att gct cgt gta cct gtt ctc		1608
Ser Glu Thr Ala Arg Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu		
295	300	305
gtc ggg acg gtg gcc aac gac gga ctt ctc ttt gtc ctc ggg gag aat		1656
Val Gly Thr Val Ala Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn		
310	315	320
gac acc caa gca tat ctc gag gag gca atc ccg aat cag ccc gac ctt		1704
Asp Thr Gln Ala Tyr Leu Glu Ala Ile Pro Asn Gln Pro Asp Leu		
325	330	335

tac cag act ctc ctt gga gca tat ccc att gga tcc cca ggg atc gga Tyr Gln Thr Leu Leu Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly 340 345 350 355	1752
tcg cct caa gat cag att gcc gcc att gag acc gag gta aga ttc cag Ser Pro Gln Asp Gln Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln 360 365 370	1800
tgt cct tct gcc atc gtg gct cag gac tcc cg <sup>g</sup> aat cg <sup>g</sup> ggt atc cct Cys Pro Ser Ala Ile Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro 375 380 385	1848
tct tgg cgc tac tac tac aat gc <sup>g</sup> acc ttt gag aat ctg gag ctt ttc Ser Trp Arg Tyr Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe 390 395 400	1896
cct ggg tcc gaa gtg tac cac agc tct gaa gtc ggg atg gtg ttt ggc Pro Gly Ser Glu Val Tyr His Ser Ser Glu Val Gly Met Val Phe Gly 405 410 415	1944
acg tat cct gtc gca agt gc <sup>g</sup> acc gcc ttg gag gcc cag acg agc aaa Thr Tyr Pro Val Ala Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys 420 425 430 435	1992
tac atg cag ggt gcc tgg gc <sup>g</sup> gcc ttt gcc aaa aac ccc atg aat ggg Tyr Met Gln Gly Ala Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly 440 445 450	2040
cct ggg tgg aaa caa gtg cc <sup>g</sup> aat gtc gc <sup>g</sup> gc <sup>g</sup> ctt ggc tca cca ggc Pro Gly Trp Lys Gln Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly 455 460 465	2088
aaa gcc atc cag gtt gac gtc tct cca gc <sup>g</sup> aca ata gac caa cga tgt Lys Ala Ile Gln Val Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys 470 475 480	2136
gcc ttg tac acg cgt tat tat act gag ttg ggc aca atc gc <sup>g</sup> cc <sup>g</sup> agg Ala Leu Tyr Thr Arg Tyr Tyr Glu Leu Gly Thr Ile Ala Pro Arg 485 490 495	2184
aca ttt ggc gga ggc agc ggc gga ggc agc ggc gga ggc agc aaa gac Thr Phe Gly Gly Ser Gly Gly Ser Gly Gly Ser Lys Asp 500 505 510 515	2232
aac gtt gc <sup>g</sup> gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg gag Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu 520 525 530	2280
acg gca cgc aaa gtc cag gcc ggc ggt ctg tcc tgc ctc gtt ctt gag Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu 535 540 545	2328
gc <sup>g</sup> atg gat cgt gta ggg gga aag act ctg agc gta caa tc <sup>g</sup> ggt ccc Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro 550 555 560	2376
ggc agg acg act atc aac gac ctc ggc gct gc <sup>g</sup> tgg atc aat gac agc Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser	2424

565	570	575	
aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly 580 585 590 595			2472
gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac ggt Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly 600 605 610			2520
aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val 615 620 625			2568
gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu 630 635 640			2616
gag cat agc cttcaa gac ctc aag gcg agc cct cag gcg aag cgg ctc Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu 645 650 655			2664
gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro 660 665 670 675			2712
gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val 680 685 690			2760
gaa gcc cac gag atc agc atg ctt ctc acc gac tac atc aag agt Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser 695 700 705			2808
gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Asp Gly Gly Gln 710 715 720			2856
tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser 725 730 735			2904
aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu 740 745 750 755			2952
att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala 760 765 770			3000
gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr Leu Tyr 775 780 785			3048
ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu 790 795 800			3096
gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg			3144

Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp			
805	810	815	
gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg			3192
Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser			
820	825	830	835
agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat			3240
Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp			
840	845	850	
cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cg aag			3288
Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys			
855	860	865	
tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa			3336
Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln			
870	875	880	
ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc			3384
Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala			
885	890	895	
aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct			3432
Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala			
900	905	910	915
ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg			3480
Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala			
920	925	930	
ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct			3528
Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser			
935	940	945	
tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga			3576
Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg			
950	955	960	
ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag			3618
Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala			
965	970	975	

<210> 29  
<211> 1205  
<212> PRT  
<213> Unknown

<220>  
<223> gst:esp1:sp:K:trAPAO

<220>  
<221> misc\_feature  
<222> (1)..(687)  
<223> gst + polylinker

<220>  
<221> misc\_feature

<222> (2191)..(2226)  
<223> spacer sequence

<220>  
<221> misc\_feature  
<222> (2227)..(3615)  
<223> K:trAPAO

<220>  
<221> misc\_feature  
<222> (2227)..(2229)  
<223> extra lysine

<400> 29

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln  
-225 -220 -215

Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu  
-210 -205 -200

His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys  
-195 -190 -185

Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp  
-180 -175 -170

Gly Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile  
-165 -160 -155

Ala Asp Lys His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala  
-150 -145 -140

Glu Ile Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly  
-135 -130 -125

Val Ser Arg Ile Ala Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val  
-120 -115 -110

Asp Phe Leu Ser Lys Leu Pro Glu Met Leu Lys Met Phe Glu Asp Arg  
-105 -100 -95

Leu Cys His Lys Thr Tyr Leu Asn Gly Asp His Val Thr His Pro Asp  
-90 -85 -80

Phe Met Leu Tyr Asp Ala Leu Asp Val Val Leu Tyr Met Asp Pro Met  
-75 -70 -65

Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys Lys Arg Ile Glu  
-60 -55 -50

Ala Ile Pro Gln Ile Asp Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala  
-45 -40 -35 -30

Trp Pro Leu Gln Gly Trp Gln Ala Thr Phe Gly Gly Asp His Pro  
-25 -20 -15

Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Glu Phe Ala Pro Thr  
-10 -5 -1 1

Val Lys Ile Asp Ala Gly Met Val Val Gly Thr Thr Thr Thr Val Pro  
5 10 15

Gly Thr Thr Ala Thr Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala  
20 25 30 35

Ser Pro Thr Arg Phe Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr  
40 45 50

Pro Leu Gln Ala Thr Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn  
55 60 65

Tyr Pro Glu Glu Leu Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro  
70 75 80

Pro Pro Ser Ala Gly Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr  
85 90 95

Val Pro Gly Thr Glu Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr  
100 105 110 115

Gly Gly Ala Leu Glu Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly  
120 125 130

Ala Ser Phe Ala Ala Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr  
135 140 145

Arg Thr Asn Ile Leu Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr  
150 155 160

Gln Arg Asn Leu Gly Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val  
165 170 175

Gln Arg Asn Ile Ala Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile  
180 185 190 195

Phe Gly Gln Ser Ala Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser  
200 205 210

Met Pro His Asn Pro Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val  
215 220 225

Ala Asn Tyr Asn Phe Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr  
230 235 240

Thr Val Gln Ala Leu Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys  
245 250 255

Met Arg Arg Val Asp Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu  
260 265 270 275

Gly Leu Gly Phe Glu Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg  
280 285 290

Ser Glu Thr Ala Arg Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu  
295 300 305

Val Gly Thr Val Ala Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn  
310 315 320

Asp Thr Gln Ala Tyr Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu  
325 330 335

Tyr Gln Thr Leu Leu Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly  
340 345 350 355

Ser Pro Gln Asp Gln Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln  
360 365 370

Cys Pro Ser Ala Ile Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro  
375 380 385

Ser Trp Arg Tyr Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe  
390 395 400

Pro Gly Ser Glu Val Tyr His Ser Ser Glu Val Gly Met Val Phe Gly  
405 410 415

Thr Tyr Pro Val Ala Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys  
420 425 430 435

Tyr Met Gln Gly Ala Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly  
440 445 450

Pro Gly Trp Lys Gln Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly  
455 460 465

Lys Ala Ile Gln Val Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys  
470 475 480

Ala Leu Tyr Thr Arg Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg  
485 490 495

Thr Phe Gly Gly Ser Gly Gly Ser Gly Gly Ser Lys Asp  
500 505 510 515

Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu  
520 525 530

Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu  
535 540 545

Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro  
550 555 560

Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser  
565 570 575

Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly  
580 585 590 595

Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly  
600 605 610

Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val  
615 620 625

Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu  
630 635 640

Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu

645

650

655

Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro  
660 665 670 675

Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val  
680 685 690

Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser  
695 700 705

Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln  
710 715 720

Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser  
725 730 735

Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu  
740 745 750 755

Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala  
760 765 770

Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr Leu Tyr  
775 780 785

Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu  
790 795 800

Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp  
805 810 815

Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser  
820 825 830 835

Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp  
840 845 850

Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys  
855 860 865

Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln  
870 875 880

Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala  
885 890 895

Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala  
900 905 910 915

Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala  
920 925 930

Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser  
935 940 945

Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg  
950 955 960

Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
965 970 975

<210> 30

<211> 3591

<212> DNA

<213> Unknown

<220>

<223> Open reading frame of BEST1:K:trAPAO fusion for bacterial expression vector pGEX-4T-1

<220>

<221> misc\_feature

<222> (1)..(687)

<223> gst + polylinker

<220>

<221> mat\_peptide

<222> (688)..(2163)

<223> BEST1 mature

<220>

<221> misc\_feature

<222> (2164)..(2199)

<223> spacer sequence

<220>

<221> misc\_feature

<222> (2200)..(3588)

<223> K:trAPAO

<220>

<221> CDS

<222> (1)...(3588)

<223>

<220>

<221> misc\_feature

<222> (2200)...(2202)

<223> extra lysine

<400> 30

atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa	45
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln	
-225 -220 -215	

ccc act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag	90
Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu	
-210 -205 -200	

cat ttg tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag	135
His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys	
-195 -190 -185	

ttt gaa ttg ggt ttg gag ttt ccc aat ctt cct tat tat att gat	180
Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp	
-180 -175 -170	

ggt gat gtt aaa tta aca cag tct atg gcc atc ata cgt tat ata	225
Gly Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile	
-165 -160 -155	

gct gac aag cac aac atg ttg ggt ggt tgt cca aaa gag cgt gca	270
Ala Asp Lys His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala	
-150 -145 -140	

gag att tca atg ctt gaa gga gcg gtt ttg gat att aga tac ggt	315
Glu Ile Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly	
-135 -130 -125	

gtt tcg aga att gca tat agt aaa gac ttt gaa act ctc aaa gtt	360
Val Ser Arg Ile Ala Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val	
-120 -115 -110	

gat ttt ctt agc aag cta cct gaa atg ctg aaa atg ttc gaa gat cgt	408
Asp Phe Leu Ser Lys Leu Pro Glu Met Leu Lys Met Phe Glu Asp Arg	
-105 -100 -95	

tta tgt cat aaa aca tat tta aat ggt gat cat gta acc cat cct gac	456
Leu Cys His Lys Thr Tyr Leu Asn Gly Asp His Val Thr His Pro Asp	
-90 -85 -80	

ttc atg ttg tat gac gct ctt gat gtt tta tac atg gac cca atg	504
Phe Met Leu Tyr Asp Ala Leu Asp Val Val Leu Tyr Met Asp Pro Met	
-75 -70 -65	

tgc ctg gat gtc cca aaa tta gtt tgt ttt aaa aaa cgt att gaa	552
Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys Lys Arg Ile Glu	
-60 -55 -50	

gct atc cca caa att gat aag tac ttg aaa tcc agc aag tat ata gca	600
---	-----

Ala Ile Pro Gln Ile Asp Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala			
-45	-40	-35	-30
tgg cct ttg cag ggc tgg caa gcc acg ttt ggt ggt ggc gac cat cct			648
Trp Pro Leu Gln Gly Trp Gln Ala Thr Phe Gly Gly Asp His Pro			
-25	-20	-15	
cca aaa tcg gat ctg gtt ccg cgt gga tcc ccg gaa ttc acg gat ttt			696
Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Glu Phe Thr Asp Phe			
-10	-5	-1 1	
ccg gtc cgc agg acc gat ctg ggc cag gtt cag gga ctg gcc ggg gac			744
Pro Val Arg Arg Thr Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp			
5 10 15			
gtg atg agc ttt cgc gga ata ccc tat gca gcg ccg cag gtc ggc ggg			792
Val Met Ser Phe Arg Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly			
20 25 30 35			
ctg cgt tgg aag ccg ccc caa cac gcc ccg ccc tgg gcg ggc gtt cgc			840
Leu Arg Trp Lys Pro Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg			
40 45 50			
ccc gcc acc caa ttt ggc tcc gac tgc ttc ggc gcg gcc tat ctt cgc			888
Pro Ala Thr Gln Phe Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg			
55 60 65			
aaa ggc agc ctc gcc ccc ggc gtg agc gag gac tgt ctt tac ctc aac			936
Lys Gly Ser Leu Ala Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn			
70 75 80			
gta tgg gcg ccg tca ggc gct aaa ccc ggc cag tac ccc gtc atg gtc			984
Val Trp Ala Pro Ser Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val			
85 90 95			
tgg gtc tac ggc ggc ttc gcc ggc acg gcc gcc atg ccc tac			1032
Trp Val Tyr Gly Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr			
100 105 110 115			
tac gac ggc gag gcg ctt gcg cga cag ggc gtc gtc gtg acg ttt			1080
Tyr Asp Gly Glu Ala Leu Ala Arg Gln Gly Val Val Val Val Thr Phe			
120 125 130			
aac tat cgg acg aac atc ctg ggc ttt ttc gcc cat cct ggt ctc tcg			1128
Asn Tyr Arg Thr Asn Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser			
135 140 145			
cgc gag agc ccc acc gga act tcg ggc aac tac ggc cta ctc gac att			1176
Arg Glu Ser Pro Thr Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile			
150 155 160			
ctc gcc gct ctt cgg tgg gtg cag acg aac gcc cgc gcc ttc gga ggg			1224
Leu Ala Ala Leu Arg Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly			
165 170 175			
gac ccc ggc cga gtg acg gtc ttt ggt gaa tcg gcc gga gcg acg gcg			1272
Asp Pro Gly Arg Val Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala			
180 185 190 195			

atc gga ctt ctg ctc acc tcg ccg ctg agc aag ggt ctc ttc cgt ggc Ile Gly Leu Leu Leu Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly	200	205	210	1320
gct atc ctc gaa agt cca ggg ctg acg cga ccg ctc gcg acg ctc gcc Ala Ile Leu Glu Ser Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala	215	220	225	1368
gac agc gcc gcc tcg ggc gag cgcc ctc gac gcc gat ctt tcg cga ctg Asp Ser Ala Ala Ser Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu	230	235	240	1416
cgc tcg acc gac cca gcc acc ctg atg gcg cgc gcc gac gcg gcc cgc Arg Ser Thr Asp Pro Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg	245	250	255	1464
ccg gca tcg cgg gac ctg cgc agg ccg cgt ccg acc gga ccg atc gtc Pro Ala Ser Arg Asp Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val	260	265	270	275
gat ggc cat gtg ctg ccg cag acc gac agc gcg gcg atc gcg gcg ggg Asp Gly His Val Leu Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly	280	285	290	1560
cag ctg gcg ccg gtt cgg gtc ctg atc gga acc aat gcc gac gaa ggc Gln Leu Ala Pro Val Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly	295	300	305	1608
cgc gcc ttc ctc ggg cgc gcg ccg atg gag acg cca gcg gac tac caa Arg Ala Phe Leu Gly Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln	310	315	320	1656
gcc tat ctg gag gcg cag ttt ggc gac caa gcc gcc gtg gcg gcg Ala Tyr Leu Glu Ala Gln Phe Gly Asp Gln Ala Ala Val Ala Ala	325	330	335	1704
tgc tat ccc ctc gac ggc cgg gcc acg ccc aag gaa atg gtc gcg cgc Cys Tyr Pro Leu Asp Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg	340	345	350	355
atc ttc ggc gac aat cag ttc aat cgg ggg gtc tcg gcc ttc tcg gaa Ile Phe Gly Asp Asn Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu	360	365	370	1800
gcg ctt gtg cgc cag ggc gcg ccc gtg tgg cgt tat cag ttc aac ggt Ala Leu Val Arg Gln Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly	375	380	385	1848
aat acc gag ggt gga aga gcg ccg gct acc cac gga gcc gaa att ccc Asn Thr Glu Gly Gly Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro	390	395	400	1896
tac gtt ttc ggg gtg ttc aag ctc gac gag ttg ggt ctg ttc gat tgg Tyr Val Phe Gly Val Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp	405	410	415	1944
ccg ccc gag ggg ccc acg ccc gcc gac cgt gcg ctg ggc caa ctg atg Pro Pro Glu Gly Pro Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met	420	425	430	435

tcc tcc gcc tgg gtc cggtt ccc gac ccc ggc ggg gac		2040	
Ser Ser Ala Trp Val Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp			
440	445	450	
 gcc ctt acc tgg cct gcc tat tct acg ggc aag tcg acc atg aca ttc		2088	
Ala Leu Thr Trp Pro Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe			
455	460	465	
 ggc ccc gag ggc cgc gcg gtgt tcg ccc gga cct tcc atc ccc		2136	
Gly Pro Glu Gly Arg Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro			
470	475	480	
 cct tgc gcg gat ggc gcc aag gcg ggg ggc gga ggc agc ggc gga ggc		2184	
Pro Cys Ala Asp Gly Ala Lys Ala Gly Gly Ser Gly Gly Gly			
485	490	495	
 agc ggc gga ggc agc aaa gac aac gtt gcg gac gtgt gta gtg gtg ggc		2232	
Ser Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val Val Gly			
500	505	510	515
 gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag gcc gcc ggt		2280	
Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly			
520	525	530	
 ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg gga aag act		2328	
Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr			
535	540	545	
 ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac gac ctc ggc		2376	
Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly			
550	555	560	
 gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc aga ttg ttt		2424	
Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe			
565	570	575	
 gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act gga aat tca		2472	
Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser			
580	585	590	595
 atc cat caa gca caa gac ggt acg acc act aca gct cct tat ggt gac		2520	
Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp			
600	605	610	
 tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc ccc		2568	
Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro			
615	620	625	
 gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag gcg		2616	
Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala			
630	635	640	
 agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg cac tac tgt		2664	
Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys			
645	650	655	
 gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca aac cag atc		2712	
Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile			

660	665	670	675	
aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc atg ctt ttt				2760
Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe				
680	685	690		
ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat att ttc tcg				2808
Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser				
695	700	705		
gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca ggt atg cag				2856
Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln				
710	715	720		
tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg cac				2904
Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His				
725	730	735		
ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc ggc tgt aca				2952
Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr				
740	745	750	755	
gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt				3000
Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val				
760	765	770		
tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct ctt				3048
Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu				
775	780	785		
ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg ggc tac tat				3096
Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr				
790	795	800		
agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa ggc				3144
Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly				
805	810	815		
ttc tcg ggc gtc ctccaa tcg agc tgt gac ccc atc tca ttt gcc aga				3192
Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg				
820	825	830	835	
gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc atg				3240
Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met				
840	845	850		
gtc gga gac ccg gga cg aag tgg tcc caa cag tcc aag cag gta cga				3288
Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg				
855	860	865		
caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc ggg				3336
Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly				
870	875	880		
gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tcg aag				3384
Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys				
885	890	895		
cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ctg aac gat				3432

Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp			
900	905	910	915
ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag agt gtt cat			3480
Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His			
920	925	930	
ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa ggg			3528
Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly			
935	940	945	
gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg gct agc ctg			3576
Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu			
950	955	960	
gtg cca gca gca tag			3591
Val Pro Ala Ala			
965			
<210> 31			
<211> 1196			
<212> PRT			
<213> Unknown			
<220>			
<223> Open reading frame of BEST1:K:trAPAO fusion for bacterial expression			
on vector pGEX-4T-1			
<220>			
<221> misc_feature			
<222> (1)..(687)			
<223> gst + polylinker			
<220>			
<221> misc_feature			
<222> (2164)..(2199)			
<223> spacer sequence			
<220>			
<221> misc_feature			
<222> (2200)..(3588)			
<223> K:trAPAO			
<220>			
<221> misc_feature			
<222> (2200)..(2202)			
<223> extra lysine			
<400> 31			
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln			
-225	-220	-215	
Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu			
-210	-205	-200	

His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys  
-195 -190 -185

Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp  
-180 -175 -170

Gly Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile  
-165 -160 -155

Ala Asp Lys His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala  
-150 -145 -140

Glu Ile Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly  
-135 -130 -125

Val Ser Arg Ile Ala Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val  
-120 -115 -110

Asp Phe Leu Ser Lys Leu Pro Glu Met Leu Lys Met Phe Glu Asp Arg  
-105 -100 -95

Leu Cys His Lys Thr Tyr Leu Asn Gly Asp His Val Thr His Pro Asp  
-90 -85 -80

Phe Met Leu Tyr Asp Ala Leu Asp Val Val Leu Tyr Met Asp Pro Met  
-75 -70 -65

Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys Lys Arg Ile Glu  
-60 -55 -50

Ala Ile Pro Gln Ile Asp Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala  
-45 -40 -35 -30

Trp Pro Leu Gln Gly Trp Gln Ala Thr Phe Gly Gly Asp His Pro  
-25 -20 -15

Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Glu Phe Thr Asp Phe  
-10 -5 -1 1

Pro Val Arg Arg Thr Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp  
5 10 15

Val Met Ser Phe Arg Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly  
20 25 30 35

Leu Arg Trp Lys Pro Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg  
40 45 50

Pro Ala Thr Gln Phe Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg  
55 60 65

Lys Gly Ser Leu Ala Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn  
70 75 80

Val Trp Ala Pro Ser Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val  
85 90 95

Trp Val Tyr Gly Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr  
100 105 110 115

Tyr Asp Gly Glu Ala Leu Ala Arg Gln Gly Val Val Val Val Thr Phe  
120 125 130

Asn Tyr Arg Thr Asn Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser  
135 140 145

Arg Glu Ser Pro Thr Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile  
150 155 160

Leu Ala Ala Leu Arg Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly  
165 170 175

Asp Pro Gly Arg Val Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala  
180 185 190 195

Ile Gly Leu Leu Leu Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly  
200 205 210

Ala Ile Leu Glu Ser Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala  
215 220 225

Asp Ser Ala Ala Ser Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu  
230 235 240

Arg Ser Thr Asp Pro Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg  
245 250 255

Pro Ala Ser Arg Asp Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val  
260 265 270 275

Asp Gly His Val Leu Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly  
280 285 290

Gln Leu Ala Pro Val Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly  
295 300 305

Arg Ala Phe Leu Gly Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln  
310 315 320

Ala Tyr Leu Glu Ala Gln Phe Gly Asp Gln Ala Ala Val Ala Ala  
325 330 335

Cys Tyr Pro Leu Asp Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg  
340 345 350 355

Ile Phe Gly Asp Asn Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu  
360 365 370

Ala Leu Val Arg Gln Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly  
375 380 385

Asn Thr Glu Gly Gly Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro  
390 395 400

Tyr Val Phe Gly Val Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp  
405 410 415

Pro Pro Glu Gly Pro Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met  
420 425 430 435

Ser Ser Ala Trp Val Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp  
440 445 450

Ala Leu Thr Trp Pro Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe  
455 460 465

Gly Pro Glu Gly Arg Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro  
470 475 480

Pro Cys Ala Asp Gly Ala Lys Ala Gly Gly Gly Ser Gly Gly Gly  
485 490 495

Ser Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val Val Gly

500 505 510 515

Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly  
520 525 530

Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr  
535 540 545

Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly  
550 555 560

Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe  
565 570 575

Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser  
580 585 590 595

Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp  
600 605 610

Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro  
615 620 625

Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala  
630 635 640

Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys  
645 650 655

Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile  
660 665 670 675

Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe  
680 685 690

Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser  
695 700 705

Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln  
710 715 720

Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His  
725 730 735

Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr

740

745

750

755

Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val  
760 765 770

Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu  
775 780 785

Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr  
790 795 800

Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly  
805 810 815

Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg  
820 825 830 835

Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met  
840 845 850

Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg  
855 860 865

Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly  
870 875 880

Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys  
885 890 895

Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp  
900 905 910 915

Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His  
920 925 930

Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly  
935 940 945

Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu  
950 955 960

Val Pro Ala Ala  
965

<210> 32  
 <211> 1803  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Glyc(-) APAO coding sequence; mutation in putative glycosylation sites

<220>  
 <221> CDS  
 <222> (1)...(1803)  
 <223>

<400> 32

atg gca ctt gca ccg agc tac atc aat ccc cca aac gtc gcc tcc cca	48
Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro	
1	5
	10
	15

gca ggg tat tct cac gtc ggc gta ggc cca gac gga ggg agg tat gtg	96
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val	
20	25
	30

aca ata gct gga cag att gga caa gac gct tcg ggc gtg aca gac cct	144
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro	
35	40
	45

gcc tac gag aaa cag gtt gcc caa gca ttc gcc aat ctg cga gct tgc	192
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys	
50	55
	60

ctt gct gca gtt gga gcc act tca aac gac gtc acc aag ctc aat tac	240
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr	
65	70
	75
	80

tac atc gtc gac tac gcc ccg agc aaa ctc acc gca att gga gat ggg	288
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly	
85	90
	95

ctg aag gct acc ttt gcc ctt gac agg ctc cct ctc acg ctg gtg	336
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val	
100	105
	110

cca gtg tcg gcc ttg tct tca cct gaa tac ctc ttt gag gtt gat gcc	384
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala	
115	120
	125

acg gcg ctg gtg ccg gga cac acg acc cca gac aac gtt gcg gac gtg	432
Thr Ala Leu Val Pro Gly His Thr Pro Asp Asn Val Ala Asp Val	
130	135
	140

gta gtg gtg ggc gct ttg agc ggt ttg gag acg gca cgc aaa gtc	480
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val	
145	150
	155
	160

cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta	528
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val	
165	170
	175

ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile 180 185 190	576
aac gac ctc ggc gct gcg tgg atc aat gat agc aat cag gcc gaa gta Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ala Glu Val 195 200 205	624
tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr 210 215 220	672
act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala 225 230 235 240	720
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala 245 250 255	768
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln 260 265 270	816
gac ctc aag gcg agc cct cag gcg aag cg <sup>g</sup> ctc gac agt gtg agc ttc Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe 275 280 285	864
g <sup>c</sup> g cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val 290 295 300	912
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile 305 310 315 320	960
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser 325 330 335	1008
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys 340 345 350	1056
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro 355 360 365	1104
g <sup>g</sup> c tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala 370 375 380	1152
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys 385 390 395 400	1200
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe	1248

405

410

415

tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile 420	425	430	1296	
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp 435	440	445	1344	
cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile 450	455	460	1392	
tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile 465	470	475	480	1440
acc tgt ttc atg gtc gga gac ccg gga aag tgg tcc caa cag tcc Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser 485	490	495	1488	
aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr 500	505	510	1536	
gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile 515	520	525	1584	
gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr 530	535	540	1632	
ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe 545	550	555	560	1680
aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly 565	570	575	1728	
tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val 580	585	590	1776	
gtg gct agc ctg gtg cca gca gca tag Val Ala Ser Leu Val Pro Ala Ala 595	600		1803	

<210> 33  
<211> 600  
<212> PRT  
<213> Unknown

<220>  
<223> Glyc(-) APAO coding sequence; mutation in putative glycosylation sites

<400> 33

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro  
1 5 10 15

Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val  
20 25 30

Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro  
35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys  
50 55 60

Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr  
65 70 75 80

Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly  
85 90 95

Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val  
100 105 110

Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala  
115 120 125

Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val  
130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val  
145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val  
165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile  
180 185 190

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ala Glu Val  
195 200 205

Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr  
210 215 220

Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala  
225 230 235 240

Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala  
245 250 255

Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln  
260 265 270

Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe  
275 280 285

Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val  
290 295 300

Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile  
305 310 315 320

Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser  
325 330 335

Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys  
340 345 350

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro  
355 360 365

Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala  
370 375 380

Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys  
385 390 395 400

Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe  
405 410 415

Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile  
420 425 430

Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp  
435 440 445

Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile  
450 455 460

Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile  
465 470 475 480

Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser  
485 490 495

Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr  
500 505 510

Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile  
515 520 525

Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr  
530 535 540

Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe  
545 550 555 560

Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly  
565 570 575

Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val  
580 585 590

Val Ala Ser Leu Val Pro Ala Ala  
595 600

<210> 34  
<211> 37  
<212> DNA  
<213> Artificial

<220>  
<223> 37-mer oligonucleotide

<400> 34  
gggaaattca tggcacttgc accgagctac atcaatc

37

<210> 35  
<211> 1929  
<212> DNA  
<213> Exophiala spinifera

<220>  
<221> Intron  
<222> (739)..(811)  
<223>

<220>  
 <221> Intron  
 <222> (1134) .. (1186)  
 <223>

<400>	35					
atgcacttg	caccgagcta	catcaatccc	ccaaacgtcg	cctccccagc	agggtattcc	60
cacatcgcg	taggccccaa	cgaagcgagg	tatgtgacaa	tagctggaca	gattggacaa	120
gacgcttgg	gcgtgacaga	cccagcctac	gagaaacagg	ttgcccaggc	attcgccaat	180
ctgcgagctt	gccttgctgc	agttggagcc	tcttcaaaccg	acgtcaccaa	gctcaattac	240
tacatcgctg	actacgcccc	gagcaaactc	accgcaattt	gagatggct	gaagtctacc	300
tttgccttg	acaggctccc	tccttgacag	ctggtgccag	taccggcctt	ggcttcacct	360
gaataacctt	ttgaggttga	tgccacggcg	ctggtgccag	gacactcgac	cccagacaac	420
gttgcggacg	tggtagtgtt	ggcgctggc	ttgagcggtt	tggagacggc	acgcaaagtc	480
caggccgccc	gtctgtcctg	cctcgttctt	gaggcgatgg	atcgtaggtt	ggaaaagact	540
ctgagcgtac	aatcgggtcc	cggcaggacg	actatcaacg	acctcgccgc	tgcgtggatc	600
aatgacagca	accaaagcga	agtatccaga	ttgtttgaaa	gatttcattt	ggagggcgag	660
ctccagagga	cgaccggaaa	ttcaatccat	caagcacaag	acggtacaac	cactacagct	720
ccttatggtg	actccccgtt	aagcacaatc	ccactttgtt	atgagacctc	tgtcgagtgt	780
agaatacagt	cactgactcc	acttcgtcca	gctgagcggag	gaggttgcaa	gtgcacttgc	840
ggaactcctc	cccgatatgg	ctcagctgtat	cgaagagtat	agccttgaag	accccaaggc	900
gagccctcag	gcgaagcggc	tcgacagtgt	gagcttcgag	cactactgtt	agaaggacct	960
aaacttgcct	gctgttctca	gcgtggcaaa	ccagatcaca	cgcgtctgc	tcgggtgtgg	1020
agcccacgag	atcagcatgc	tttttctcac	cgactacatc	aagagtgcac	ccgggtctcag	1080
taatattgtc	tcggacaaga	aagacggcgg	gcagtatatg	cgatgaaaaa	caggtgcgtg	1140
cgggtcctc	tcaggttaggg	gactcggttc	ttagtggtca	ttccaggtat	gcagtcgatt	1200
tgccatgcca	tgtcaaagga	acttggtcca	ggctcagtgc	acctcaacac	ccccgtcgct	1260
ggaattgagc	agtcggcgcc	cggctgtata	gtacgatcg	cctcggggcgc	cgtgttccga	1320
agcaaaaagg	tggtggttcc	gttaccgaca	acattgtatc	ccaccttgcac	attttaccca	1380
cctcttcccg	ccgagaagca	agcattggcg	gaaaaatcta	tcctcggtca	ctatagcaag	1440
atagtcttcg	tatggacaa	cccgtgggg	cgcgaacaag	gcttctcggt	cgtcctccaa	1500
tcgagctgtg	accccatctc	atttgccaga	gataccagca	tcgaagtcga	tcggcaatgg	1560
tccattacct	gtttcatgg	cggagaccccg	ggacgaaagt	ggtcccaaca	gtccaaagcag	1620

gtacgacaaa agtctgtctg ggaccaactc cgcgagcc acgagaacgc cggggccaa 1680  
gtcccagagc cggccaacgt gctcgaaatc gagtggtcga agcagcagta tttccaagga 1740  
gctccgagcg ccgtctatgg gctgaacgtat ctcacac tgggttcggc gctcagaacg 1800  
ccgttcaagt gtgttcattt cggttggaaacg gagacgtctt tagttggaa agggtatatg 1860  
gaaggggcca tacgatcggg tcaacgaggt gctgcagaag ttgtggctag cctggtgcca 1920  
gcagcatag 1929

<210> 36  
<211> 600  
<212> PRT  
<213> Exophilia spinifera

<400> 36

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro  
1 5 10 15

Ala Gly Tyr Ser His Ile Gly Val Gly Pro Asn Glu Ala Arg Tyr Val  
20 25 30

Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Leu Gly Val Thr Asp Pro  
35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys  
50 55 60

Leu Ala Ala Val Gly Ala Ser Ser Asn Asp Val Thr Lys Leu Asn Tyr  
65 70 75 80

Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly  
85 90 95

Leu Lys Ser Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val  
100 105 110

Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala  
115 120 125

Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val  
130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val  
145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val  
165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile  
180 185 190

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val  
195 200 205

Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr  
210 215 220

Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala  
225 230 235 240

Pro Tyr Gly Asp Ser Pro Leu Ser Glu Glu Val Ala Ser Ala Leu Ala  
245 250 255

Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu Tyr Ser Leu Glu  
260 265 270

Asp Pro Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe  
275 280 285

Ala His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Ser Val  
290 295 300

Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile  
305 310 315 320

Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser  
325 330 335

Asn Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys  
340 345 350

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro  
355 360 365

Gly Ser Val His Leu Asn Thr Pro Val Ala Gly Ile Glu Gln Ser Ala  
370 375 380

Ser Gly Cys Ile Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys

385                   390                   395                   400

Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe  
405    410                                  415

Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile  
420    425                                  430

Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Asn Pro Trp Trp  
435    440                                  445

Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile  
450    455                                  460

Ser Phe Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile  
465    470                                  480

Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser  
485    490                                  495

Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr  
500    505                                  510

Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile  
515    520                                  525

Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr  
530    535                                  540

Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe  
545    550                                  560

Lys Cys Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly  
565    570                                  575

Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val  
580    585                                  590

Val Ala Ser Leu Val Pro Ala Ala  
595    600

<210> 37  
<211> 1929  
<212> DNA  
<213> Exophiala spinifera

<220>  
 <221> Intron  
 <222> (739) .. (811)  
 <223>

<220>  
 <221> Intron  
 <222> (1134) .. (1186)  
 <223>

<400> 37

atggcacttg	caccgagcta	catcaatccc	ccaaacgtcg	cctccccagc	agggtattcc	60
cacatcgccg	taggccccaaa	cgaagcgagg	tatgtgacaa	tagctggaca	gattggacaa	120
gacgcgttgg	gcgtgacaga	cccagcctac	gagaaacagg	ttgccccagg	attcgccaaat	180
ctgcgagctt	gccttgctgc	agttggagcc	tcttcaaacs	acgtcaccaa	gctcaattac	240
tacatcgctg	actacgcccc	gagcaaactc	accgcaattg	gagatgggct	gaagtctacc	300
tttgccttg	acaggctccc	tccttgacag	ctgggtgccag	taccggcctt	ggcttcaccc	360
gaataacctct	ttgaggttga	cggcacggcg	ctgggtgccag	gacactcgac	cccagacaac	420
gttgcggacg	tggtagtgtt	ggcgctggc	ttgagcggct	tggagacggc	acgcaaagtc	480
caggccgccc	gtctgtcctg	cctcgtttctt	gaggcgatgg	atcgtgttagg	gggaaagact	540
ctgagcgtac	aatcgggtcc	cggcaggacg	actatcaacg	acctcgccgc	tgcgtggatc	600
aatgacagca	accaaagcga	agtatccaga	ttgtttgaaa	gatttcattt	ggagggcgag	660
ctccagagga	cgaccggaaa	ttcaatccat	caagcacaag	acggtacaac	cactacagct	720
ccttatggtg	actccccgt	aagcacaatc	ccactttgtg	atgagacctc	tgtcgagtgt	780
agaatacagt	cactgactcc	acttcgtcca	gctgagcgag	gaggttgcaa	gtgcacttgc	840
ggaactcctc	cccgatgtgt	ctcagctgat	cgaagagtat	agccttgaag	accccaaggc	900
gagccctcag	gcgaagcgcc	tcgacagtgt	gagcttcgcg	cactactgtg	agaaggacct	960
aaacttgcct	gctgttctca	gcgtggcaaa	ccagatcaca	cgcgtctgc	tcgggtgtgga	1020
agcccacgag	atcagcatgc	tttttctcac	cgactacatc	aagagtgcc	ccggctctcag	1080
taatattgtc	tcggacaaga	aagacggcg	gcagtatatg	cgatgaaaaa	caggtgcgtg	1140
cggtgtcctc	tcaggttaggg	gactcggttc	ttagtggtca	ttccaggtat	gcagtcgatt	1200
tgccatgcca	tgtcaaagga	acttggtcca	ggctcagtgc	acctcaacac	ccccgtcgct	1260
ggaattgagc	agtcggcgtc	cggctgtata	gtacgatcg	cctcgccgc	cgtgttccga	1320
agcaaaaagg	tggtggttgc	gttaccgaca	acattgtatc	ccaccttgac	attttccacca	1380
cctcttcccg	ccgagaagca	agcattggcg	gaaaaatcta	tcctcggtca	ctatagcaag	1440

atagtcttcg tatggacaa cccgtggtgg cgcgaaacaag gcttctcggg cgtcctccaa 1500  
tcgagctgtg accccatctc atttgccaga gataccagca tcgaagtcga tcggcaatgg 1560  
tccattacct gttcatggt cggagacccg ggacggaagt ggtcccaaca gtccaaggcag 1620  
gtacgacaaa agtctgtctg ggaccaactc cgcgacgc acgagaacgc cggggcccaa 1680  
gtcccagagc cggccaacgt gctcgaaatc gagtggtcga agcagcagta tttccaagga 1740  
gctccgagcg ccgtctatgg gctgaacgtat ctcacac tgggttcggc gctcagaacg 1800  
ccgttcaagt gtgttcattt cgttggAACg gagacgtctt tagttggaa agggtatatg 1860  
gaaggggcca tacgatcggg tcaacgaggt gctgcagaag ttgtggctag cctggtgcca 1920  
gcagcatag 1929

<210> 38  
<211> 600  
<212> PRT  
<213> Exophiala spinifera

<400> 38

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro  
1 5 10 15

Ala Gly Tyr Ser His Ile Gly Val Gly Pro Asn Glu Ala Arg Tyr Val  
20 25 30

Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Leu Gly Val Thr Asp Pro  
35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys  
50 55 60

Leu Ala Ala Val Gly Ala Ser Ser Asn Asp Val Thr Lys Leu Asn Tyr  
65 70 75 80

Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly  
85 90 95

Leu Lys Ser Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val  
100 105 110

Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala  
115 120 125

Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val  
130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val  
145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val  
165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile  
180 185 190

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val  
195 200 205

Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr  
210 215 220

Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala  
225 230 235 240

Pro Tyr Gly Asp Ser Pro Leu Ser Glu Glu Val Ala Ser Ala Leu Ala  
245 250 255

Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu Tyr Ser Leu Glu  
260 265 270

Asp Pro Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe  
275 280 285

Ala His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Ser Val  
290 295 300

Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile  
305 310 315 320

Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser  
325 330 335

Asn Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys  
340 345 350

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro  
355 360 365

Gly Ser Val His Leu Asn Thr Pro Val Ala Gly Ile Glu Gln Ser Ala  
370 375 380

Ser Gly Cys Ile Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys  
385 390 395 400

Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe  
405 410 415

Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile  
420 425 430

Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Asn Pro Trp Trp  
435 440 445

Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile  
450 455 460

Ser Phe Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile  
465 470 475 480

Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser  
485 490 495

Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr  
500 505 510

Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile  
515 520 525

Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr  
530 535 540

Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe  
545 550 555 560

Lys Cys Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly  
565 570 575

Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val  
580 585 590

Val Ala Ser Leu Val Pro Ala Ala  
595 600

<210> 39  
<211> 1930  
<212> DNA  
<213> Exophiala spinifera

<220>  
<221> Intron  
<222> (739) .. (811)  
<223>

<220>  
<221> Intron  
<222> (1134) .. (1187)  
<223>

<220>  
<221> misc\_feature  
<222> (649) .. (649)  
<223> n = A,T,C or G

<400> 39  
atggcacttg caccgagcta catcaatccc ccaaacgtcg cctccccagc agggtattct 60  
cacgtcggcg taggcccaga cgaggaggagg tatgtgacaa tagctggaca gattggacaa 120  
gacgcttcgg gcgtgacaga ccctgcctac gagaaacagg ttgccccaaagc attcgccaat 180  
ctgcgagctt gccttgcgtc agttggagcc acttcaaaca acgtcaccaa gctcaattac 240  
tacatcgctcg actacgcccc gagcaaactc accgcaattt gагатgggct gaaggctacc 300  
tttgccttg acaggctccc tccttgcacg ctggtgccag tgtcggcctt gtcttacacct 360  
gaataacctct ttgaggttga tgccacggcg ctggtgccgg gacacacgac cccagacaac 420  
gttgcggacg tggtagtggt gggcgctggc ttgagcgggtt tggagacggc acgcaaagtc 480  
caggccgccc gtctgtcctg cctcgttctt gaggcgatgg atcgtgttagg gggaaagact 540  
ctgagcgtac aatcgggtcc cggcaggacg actatcaacg acctcggcgc tgcgtggatc 600  
aatgacagca accaaagcga agtatccaga ttgtttgaaa gatttcatnt ggagggcgag 660  
ctccagagga cgactggaaa ttcaatccat caagcacaag acggtacaac cactacagct 720  
ccttatggtg actccttggt aagcacaatc ccactttgtg atgagacctc tgtcgagtgt 780  
agaatacagt cactgattcc acttcgtcca gctgagcggag gaggttgcaa gtgcacttgc 840  
ggaactcctc cccgtatggc ctcagctgat cgaagagcat agccttcaag acctcaaggc 900  
gagccctcag gcgaaggcgc tcgacagtgt gagcttcgcg cactactgtg agaaggaact 960  
aaacttgccct gctgttctcg gcgttagcaaa ccagatcaca cgcgcctctgc tcggtgtgga 1020  
agcccacgag atcagcatgc tttttctcac cgactacatc aagagtgccaa ccggctctcag 1080

taatattttc tcggacaaga aagacggcg gcagtatatg cgatgcaaaa caggtgcgtg 1140  
tgggtcgtc tcaggtgggg gactcgtttc tcaagtggtc atttcaggta tgcagtcgat 1200  
ttgccatgcc atgtcaaagg aacttgtcc aggctcagtg cacctaaca cccccgtcgc 1260  
tgaaatttag cagtcggcat ccggctgtac agtacgatcg gcctcggcg ccgtgttccg 1320  
aagcaaaaag gtggtggttt cgttaccgac aaccttgtat cccaccttga cattttcacc 1380  
acctctcccc gccgagaagc aagcattggc ggaaaattct atcctggct actatacgaa 1440  
gatagtcttc gtatggaca agccgtggtgcgcgaacaa ggcttctcg gcgtcctcca 1500  
atcgagctgt gacccatct catttgcag agataccagc atcgacgtcg atcgacaatg 1560  
gtccattacc tgtttcatgg tcggagaccc gggacggaag tggtccaaac agtccaagca 1620  
ggtacgacaa aagtctgtct gggaccaact ccgcgcagcc tacgagaacg ccggggccca 1680  
agtcccagag ccggccaacg tgctcgaaat cgagtggtcg aagcagcagt atttccaagg 1740  
agctccgagc gccgtctatg ggctgaacga tctcatcaca ctgggttcgg cgctcagaac 1800  
gccgttcaag agtgttcatt tcgttggAAC ggagacgtct ttagttggaa aagggttat 1860  
ggaaggggcc atacgatcggtcaacgagg tgctgcagaa gttgtggcta gcctgggcc 1920  
agcagcatag 1930

<210> 40  
<211> 598  
<212> PRT  
<213> Exophiala spinifera

<220>  
<221> MISC\_FEATURE  
<222> (216)..(216)  
<223> Xaa = any amino acid

<400> 40

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro  
1 5 10 15

Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val  
20 25 30

Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro  
35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys  
50 55 60

Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr  
65 70 75 80

Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly  
85 90 95

Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val  
100 105 110

Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala  
115 120 125

Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val  
130 135 140

Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln  
145 150 155 160

Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly  
165 170 175

Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn  
180 185 190

Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser  
195 200 205

Arg Leu Phe Glu Arg Phe His Xaa Glu Gly Glu Leu Gln Arg Thr Thr  
210 215 220

Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro  
225 230 235 240

Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu  
245 250 255

Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp  
260 265 270

Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala  
275 280 285

His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Asn  
100

290

295

300

Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met  
305 310 315 320

Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile  
325 330 335

Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly  
340 345 350

Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser  
355 360 365

Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly  
370 375 380

Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val  
385 390 395 400

Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro  
405 410 415

Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly  
420 425 430

Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu  
435 440 445

Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe  
450 455 460

Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys  
465 470 475 480

Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln  
485 490 495

Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn  
500 505 510

Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp  
515 520 525

Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu  
530 535 540

Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser  
545 550 555 560

Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met  
565 570 575

Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala  
580 585 590

Ser Leu Val Pro Ala Ala  
595

<210> 41  
<211> 1928  
<212> DNA  
<213> Rhinocladiella atrovirens

<220>  
<221> Intron  
<222> (739)..(811)  
<223>

<220>  
<221> Intron  
<222> (1134)..(1185)  
<223>

<400> 41  
atggcacttg caccgagcta catcaatccc ccaaaccctcg cctcccccagc agggtattcc 60  
cacgtcggcg taggccccaa cggagggagg tatgcgacaa tagctggaca gattggacaa 120  
gacgcttcgg ccgtgacaga ccctgcctac gagaaacagg ttgcccagg attcgccaac 180  
ctgcgagctt gtcttgctgc agttggagcc acttcaaacg acattaccaa gctcaattac 240  
tacatcgctcg actacaaccc gagcaaactc accgcaattt gagatggct gaaggctacc 300  
tttgccttg acaggctccc tccttgacag ctggtgccag tgccggccct ggcttcacct 360  
gaataccccc ttgaggttga tgccacggcg ctggttccag gacactcaac cccagacaat 420  
gttgcggacg tggtcgtggt gggcgctggc ttgagcgggt tggagacggc acgcaaagtc 480  
caggctgccg ggctgtcctg cctcgttttt gaggcgatgg atcgtgtggg gggaaagact 540  
ctgagcgtac aatcggttcc cggcaggacg gctatcaatg acctcgccgc tgcgtggatc 600  
aatgacagca accaaagcga agtattcaaa ttatggaaa gatttcattt ggagggcgag 660  
ctccagagga cgaccggaaa ttcaatccat caagcacaag acggtacaac cactacagct 720

ccttatggtg	attccctggt	aagcacaatt	ccatcttgc	atgagacctc	tgtcggtgt	780
agaatacagt	cgctgactcc	acatcgcca	gctgagcgag	gaggttgcaa	gtgcactcg	840
ggaactcctt	cccgcatggt	ctcagctgat	cgaagagcat	agtcttgaag	accccaaggc	900
gagccctcaa	gcgaaggcgc	tcgacagtgt	gagcttcgca	cactactgtg	agaaggatct	960
aagcttgcct	gctgttctcg	gcgtggcaaa	ccagatcaca	cgcgctctgc	tcgggtgtgga	1020
agcccacgag	atcagcatgc	tttttctcac	cgactacatc	aagagtgc	ccgggtctcag	1080
taatattgtc	tcggataaga	aagacggtgg	gcagtatatg	cgatgc	aaaaa caggtgcgtg	1140
tgggtttctc	tcagtggag	actcgtttct	tagtggtcat	tccaggtatg	cagtcgttt	1200
gccatgccat	gtcaaaggaa	cttgttccag	gctcagtgc	cctcaacacc	cccgtcgccg	1260
aaattgagca	gtcggcatcc	ggctgtacag	tacgatcg	ctcgggcggc	gtgttccgaa	1320
gtaaaaaggt	ggtggtttcg	ttaccgacaa	ccttgtatcc	caccttgata	ttttcaccac	1380
ctcttcccgc	cgagaagcaa	gcattggctg	aaaaatccat	cctgggctac	tatagcaaga	1440
tagtcttcgt	atgggacaag	ccgtggtggc	gcgaacaagg	cttctcggc	gtcctccaa	1500
cgagctgtga	ccccatctca	tttgcagag	ataccagcat	cgaagtgc	atcggttt	1560
ccattacctg	tttcatggtc	ggagacccgg	gacgaaagtg	gtcccaacag	tccaa	1620
tacgacagaa	gtctgtctgg	aaccaactcc	g	cgcaacgc	ggggcccaag	1680
tccca	ggccaaacgtg	ctcgagatcg	agtggtc	g	caaggat	1740
cgccgagcgt	cgtctatggg	ctgaactgc	tcaacacact	gggttcggc	ctcagaacgc	1800
cgttcaagg	tgttcatttc	gttggAACGG	agacgtctt	ggtttgaaa	gggttatatgg	1860
aaggggccat	acgatcggt	cagcgaggcg	ctgcaga	gtgtggctagc	ctgggtccag	1920
cagcatag						1928

<210> 42  
 <211> 598  
 <212> PRT  
 <213> Rhinocladiella atrovirens

<400> 42

Met	Ala	Leu	Ala	Pro	Ser	Tyr	Ile	Asn	Pro	Pro	Asn	Leu	Ala	Ser	Pro
1				5				10				15			

Ala	Gly	Tyr	Ser	His	Val	Gly	Val	Gly	Pro	Asn	Gly	Gly	Arg	Tyr	Ala
20					25							30			

Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Ala Val Thr Asp Pro  
35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys  
50 55 60

Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr  
65 70 75 80

Tyr Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly  
85 90 95

Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val  
100 105 110

Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Pro Phe Glu Val Asp Ala  
115 120 125

Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val  
130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val  
145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val  
165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Ala Ile  
180 185 190

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val  
195 200 205

Phe Lys Leu Phe Glu Arg Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly  
210 215 220

Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr  
225 230 235 240

Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu  
245 250 255

Leu Pro Ala Trp Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp Pro  
260 265 270

Lys Ala Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala His  
275 280 285

Tyr Cys Glu Lys Asp Leu Ser Leu Pro Ala Val Leu Gly Val Ala Asn  
290 295 300

Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met  
305 310 315 320

Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile  
325 330 335

Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly  
340 345 350

Met Gln Ser Leu Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser  
355 360 365

Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly  
370 375 380

Cys Thr Val Arg Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys Val  
385 390 395 400

Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Ile Phe Ser Pro  
405 410 415

Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile Leu Gly  
420 425 430

Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu  
435 440 445

Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe  
450 455 460

Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile Thr Cys  
465 470 475 480

Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln  
485 490 495

Val Arg Gln Lys Ser Val Trp Asn Gln Leu Arg Ala Ala Tyr Glu Asn  
500 505 510

Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp  
515 520 525

Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Val Val Tyr Gly Leu  
530 535 540

Asn Cys Leu Asn Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Gly  
545 550 555 560

Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met  
565 570 575

Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala  
580 585 590

Ser Leu Val Pro Ala Ala  
595

<210> 43  
<211> 1928  
<212> DNA  
<213> Rhinocladiella atrovirens

<220>  
<221> Intron  
<222> (739)..(811)  
<223>

<220>  
<221> Intron  
<222> (1134)..(1186)  
<223>

<400> 43  
atggcacttg caccgagcta catcaatccc ccaaacctcg cctccccagc agggtattcc 60  
tacgtcggcg taggccccaa cgaggaggagg tatgtgacaa tagctggaca gattggacaa 120  
gacgcttcgg ccgtgacaga ccctgcctac gagaaacagg ttgcccagg attcgccaac 180  
ctgcgagctt gtcttgctgc agttggagcc acttcaaacg acattaccaa gctcaattac 240  
tacatcgctg actacaaccc gagcaaactc accgcaattg gagatggctt gaaggctacc 300  
tttgccttg acaggctccc tccttgacag ctggtgccag tgccggccct ggcttcacct 360  
gaataacctct ttgaggttga tgccacggcg ctgggtccag gacactcaac cccagacaat 420  
gttgcggacg tggtcgttgtt gggcgctggc ttgagcggtt tggagacggc acgcaaagtc 480  
caggctgccc ggctgtcctg cctcgatctt gaggcgatgg atcgtgtggg gggaaagact 540

ctgagcgtac	aatcggtcc	cggcaggacg	actatcaatg	acctcggcgc	tgcgtggatc	600
aatgacagca	accaaagcga	agtattcaa	ttatggaaa	gatttcattt	ggagggcgg	660
ctccagagga	cgaccggaaa	ttcaatccat	caagcacaag	acggtacaac	cactacagct	720
ccttatggtg	attcccttgtt	aagcacaatt	ccatcttgt	atgagacctc	tgtcgtgtgt	780
agaatacagt	cgctgactcc	acatcgcca	gctgagcgg	gagggtgcaa	gtgcactcgc	840
ggaactcctt	cccgcatgg	ctcagctgat	cgaagagcat	agtcttgaag	accccaaggc	900
gagccctcaa	gcgaaggcgc	tcgacagtgt	gagcttcga	cactactgt	agaaggatct	960
aaacttgcct	gctgttctcg	gcgtggcaaa	ccagatcaca	cgcgctctgc	tcgggtggaa	1020
agcccacgag	atcagcatgt	tttttctcac	cgactacatc	aagagtgc	ccgggtctcag	1080
taatattgtc	tcggataaga	aagacggtgg	gcagtatatg	cgatgc	aaaaaa caggtgcgtg	1140
tgggtttctc	tcagtggag	actcgttct	tagtggtcat	tccaggat	cagtcgc	1200
gccatgccat	gtcaaaggaa	cttggccag	gctcagtgc	cctcaacacc	cccgtcgccg	1260
aaatttagca	gtcgccatcc	ggctgtacag	tacgatggc	ctcgccggc	gtgttccgaa	1320
gtaaaaaggt	ggtggtttcg	ttaccgacaa	ccttgc	atcc	cacccgtata	1380
ctcttccgc	cgagaagcaa	gcattggctg	aaaaatccat	cctggctac	tatagcaaga	1440
tagtcttcgt	atgggacaag	ccgtggtggc	gcgaacaagg	cttctcgccg	gtcctccaa	1500
cgagctgtga	ccccatctca	tttgcagag	ataccagcat	cgaagtgc	cgcaatgg	1560
ccattacctg	tttcatggc	ggagacccgg	gacggaaatg	gtcccaacag	tccaaagg	1620
tacgacagaa	gtctgtctgg	aaccaactcc	gcgcagccta	cgagaacg	ccccaa	1680
tcccaagagcc	ggccaaacgtg	ctcgagatcg	agtggtcgaa	gcagcgtat	ttccaaggag	1740
cgcgcgcgc	cgtctatgg	ctgaactgtc	tcaacacact	gggttcggcg	ctcagaacgc	1800
cgttcaaggg	tgttcat	ttcgttggaa	agacgtctt	ggtttgaaa	gggtatatgg	1860
aaggggccc	atcgatcggt	cagcgaggcg	ctgcagaagt	tgtggctagc	ctgggtccag	1920
cagcatag						1928

<210> 44  
 <211> 591  
 <212> PRT  
 <213> Rhinocladiella atrovirens

<400> 44

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Leu Ala Ser Pro  
 1 5 10 15

Ala Gly Tyr Ser Tyr Val Gly Val Gly Pro Asn Gly Gly Arg Tyr Val  
20 25 30

Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Ala Val Thr Asp Pro  
35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys  
50 55 60

Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr  
65 70 75 80

Tyr Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly  
85 90 95

Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val  
100 105 110

Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala  
115 120 125

Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val  
130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val  
145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val  
165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Gly Arg Thr Thr Ile Asn  
180 185 190

Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Lys  
195 200 205

Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly  
210 215 220

Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr  
225 230 235 240

Gly Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu

245

250

255

Pro Ala Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp Pro Lys Ala  
260 265 270

Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala His Tyr Cys  
275 280 285

Glu Lys Leu Asn Leu Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg  
290 295 300

Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Phe Phe Leu Thr  
305 310 315 320

Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Val Ser Asp Lys  
325 330 335

Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Leu  
340 345 350

Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn  
355 360 365

Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg  
370 375 380

Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys Val Val Leu Pro Thr  
385 390 395 400

Leu Tyr Pro Thr Leu Ile Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln  
405 410 415

Ala Leu Ala Glu Lys Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe  
420 425 430

Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu  
435 440 445

Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Glu  
450 455 460

Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly  
465 470 475 480

Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp  
485 490 495

Asn Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu  
500 505 510

Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln  
515 520 525

Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Cys Leu Asn Thr Leu Gly  
530 535 540

Ser Ala Leu Arg Thr Pro Phe Lys Gly Val His Phe Val Gly Thr Glu  
545 550 555 560

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly  
565 570 575

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
580 585 590

<210> 45  
<211> 1928  
<212> DNA  
<213> Rhinocladiella atrovirens

<220>  
<221> Intron  
<222> (739)..(811)  
<223>

<220>  
<221> Intron  
<222> (1134)..(1185)  
<223>

<400> 45  
atggcacttg caccgagcta catcaatccc ccaaaccctcg cctcccccagc agggtattcc 60  
cacgtcgccg taggccaaa cgaggaggagg tatgtgacaa tagctggaca gattggacaa 120  
gacgcttcgg ccgtgacaga ccctgcctac gagaaacagg ttgccccagg attcgccaac 180  
ctgcgagctt gtcttgctgc agttggagcc acttcaaacg acattaccaa gctcaattac 240  
tacatcgctcg actacaaccc gagcaaactc accgcaattg gagatggct gaaggctacc 300  
tttgccttg acaggctccc tccttgcacg ctggtgccag tgccggccct ggcttcacct 360  
gaataacctct ttgaggttga tgctacggcg ctggttccag gacactcaac cccagacaat 420  
gttgcggacg tggtcgtgg gggcgctggc ttgagcgggt tggagacggc acgcaaagtc 480

caggctgccg ggctgtcctg cctcgttctt gaggcgatgg atcgtgtggg gggaaagact	540
ctgagcgtac aatcggtcc cgccaggacg actatcaatg acctcggcgc tgcgtggatc	600
aatgacagca accaaagcga agtattcaa ttatttggaa gatttcattt ggagggcgag	660
ctccagagga cgaccggaaa ttcaatccat caagcacaag acggtaaac cactacagct	720
ccttatggtg attcccttgtt aggccaaatt ccattttgtg atgagacac tcgtgtgt	780
agaatacagt cgctgactcc acatcgcca gctgagcgag gaggttgcaa gtgcactcgc	840
ggaactcctt cccgcattgtt ctcaatgtat cgaagagcat agtcttgaag accccaaggc	900
gagccctcaa gcgaaggcgc tcgacagtgt gagcttcgca cactactgtg agaaggatct	960
aaacttgcct gctgttctcg gcgtggcaaa ccagatcaca cgcgcctctgc tcgggtgtga	1020
agccccacgag atcagcatgc ttttctcac cgactacatc aagagtgcac ccggctctcag	1080
taatattgtc tcggataaga aagacggtgg gcagtatatg cgatgcacaa caggtgcgtg	1140
tgggtttctc tcagtggag actcgttct tagtggtcat tccaggtatg cagtcgttt	1200
ccatgccat gtcaaaggaa cttgttccag gctcagtgca cctcaacacc cccgtcgccg	1260
aaatttagca gtcggcatcc ggctgtacag tacgatcgcc ctggggcgcc gtgttccgaa	1320
gtaaaaaggt ggtggtttcg ttaccgacaa cttgttatcc caccttgata ttttaccac	1380
ctcttcccgc cgagaagcaa gcattggctg aaaaatccat cctgggctac tatagcaaga	1440
tagtcttcgt atgggacaag ctgtggtggc gcgaacaagg cttctcgcc gtcctccat	1500
cgagctgtga ccccatctca tttgccagag ataccagcat cgaagtcgtat cggcaatgg	1560
ccattacctg tttcatggtc ggagacccgg gacggaaatg gtcctcaacag tccaaagg	1620
tacgacagaa gtctgtctgg aaccaactcc ggcgcgccta cgagaacgccc ggggccccaa	1680
tcccgagcc ggccaaacgtg ctcgagatcg agtggtcgaa gcagcgtat ttccaaggag	1740
cgccgagcgc cgtctatggg ctgaactgtc tcaacacact gggttcgccg ctcagaacgc	1800
cgttcaaggg tggttcatatc gttggAACGG agacgtcttt gggttggaaa gggtatatgg	1860
aaggggccat acgatcggt cagcgaggcg ctgcagaatgt tgcgttagc ctgggtgccag	1920
cagcatag	1928

<210> 46  
 <211> 591  
 <212> PRT  
 <213> Rhinocladiella atrovirens

<400> 46

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Ala Ser Pro Ala  
1 5 10 15

Gly Tyr Ser His Val Gly Val Gly Pro Asn Gly Gly Arg Tyr Val Thr  
20 25 30

Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Ala Val Thr Asp Pro Ala  
35 40 45

Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys Leu  
50 55 60

Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr Tyr  
65 70 75 80

Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly Leu  
85 90 95

Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val Pro  
100 105 110

Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala Thr  
115 120 125

Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val Val  
130 135 140

Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln  
145 150 155 160

Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly  
165 170 175

Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn  
180 185 190

Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Phe  
195 200 205

Lys Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr  
210 215 220

Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro  
225 230 235 240

Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu  
245 250 255

Leu Leu Pro Ala Trp Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp  
260 265 270

Pro Lys Ala Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala  
275 280 285

His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Gly Val Ala  
290 295 300

Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser  
305 310 315 320

Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn  
325 330 335

Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr  
340 345 350

Gly Met Gln Ser Leu Cys His Ala Met Ser Lys Glu Leu Val Pro Gly  
355 360 365

Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser  
370 375 380

Gly Cys Thr Val Arg Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys  
385 390 395 400

Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Ile Phe Ser Pro Leu  
405 410 415

Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile Gly Tyr Tyr Ser  
420 425 430

Lys Ile Val Phe Val Asp Lys Leu Trp Trp Arg Glu Gln Gly Phe Ser  
435 440 445

Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr  
450 455 460

Ser Ile Glu Val Asp Arg Gln Ser Ile Thr Cys Phe Met Val Gly Asp  
465 470 475 480

Pro Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val  
485 490 495

Trp Asn Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro  
500 505 510

Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe  
515 520 525

Gln Ala Pro Ser Ala Val Tyr Gly Leu Asn Cys Leu Asn Thr Leu Gly  
530 535 540

Ser Ala Leu Arg Thr Pro Phe Lys Gly Val His Phe Val Gly Thr Glu  
545 550 555 560

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly  
565 570 575

Gln Arg Gly Ala Ala Glu Val Val Pro Ser Leu Val Pro Ala Ala  
580 585 590

<210> 47  
<211> 600  
<212> PRT  
<213> Exophiala spinifera

<400> 47

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro  
1 5 10 15

Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val  
20 25 30

Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro  
35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys  
50 55 60

Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr  
65 70 75 80

Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly  
85 90 95

Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val  
100 105 110

Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala  
115 120 125

Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val  
130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val  
145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val  
165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile  
180 185 190

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val  
195 200 205

Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr  
210 215 220

Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala  
225 230 235 240

Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala  
245 250 255

Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln  
260 265 270

Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe  
275 280 285

Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val  
290 295 300

Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile  
305 310 315 320

Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser

325

330

335

Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys  
340 345 350

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro  
355 360 365

Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala  
370 375 380

Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys  
385 390 395 400

Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe  
405 410 415

Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile  
420 425 430

Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp  
435 440 445

Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile  
450 455 460

Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile  
465 470 475 480

Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser  
485 490 495

Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr  
500 505 510

Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile  
515 520 525

Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr  
530 535 540

Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe  
545 550 555 560

Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly  
565 570 575

Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val  
580 585 590

Val Ala Ser Leu Val Pro Ala Ala  
595 600

<210> 48  
<211> 1392  
<212> DNA  
<213> Unknown

<220>  
<223> Cys (-) APAO; removal of cysteine 461

<220>  
<221> CDS  
<222> (1)..(1392)  
<223>

<400> 48  
aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt 48  
Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly  
1 5 10 15  
  
ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt 96  
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val  
20 25 30  
  
ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg 144  
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser  
35 40 45  
  
ggc ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat 192  
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn  
50 55 60  
  
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg 240  
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu  
65 70 75 80  
  
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa 288  
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln  
85 90 95  
  
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag 336  
Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu  
100 105 110  
  
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg 384  
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu  
115 120 125  
  
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag 432

Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys			
130	135	140	
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac		480	
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn			
145	150	155	160
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc		528	
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu			
165	170	175	
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc		576	
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile			
180	185	190	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc		624	
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly			
195	200	205	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc		672	
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala			
210	215	220	
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc		720	
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val			
225	230	235	240
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg		768	
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser			
245	250	255	
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc		816	
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr			
260	265	270	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa		864	
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln			
275	280	285	
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc		912	
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe			
290	295	300	
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc		960	
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu			
305	310	315	320
caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac		1008	
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp			
325	330	335	
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga		1056	
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly			
340	345	350	
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg		1104	
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp			
355	360	365	

gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag 1152  
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu  
370 375 380

ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa 1200  
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln  
385 390 395 400

gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt 1248  
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly  
405 410 415

tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag 1296  
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu  
420 425 430

acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt 1344  
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly  
435 440 445

caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag 1392  
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
450 455 460

<210> 49

<211> 463

<212> PRT

<213> Unknown

<220>

<223> Cys (-) APAO; removal of cysteine 461

<400> 49

Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly  
1 5 10 15

Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val  
20 25 30

Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser  
35 40 45

Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn  
50 55 60

Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu  
65 70 75 80

Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln  
85 90 95

Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu  
100 105 110

Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu  
115 120 125

Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys  
130 135 140

Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn  
145 150 155 160

Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu  
165 170 175

Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile  
180 185 190

Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly  
195 200 205

Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala  
210 215 220

Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val  
225 230 235 240

Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser  
245 250 255

Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr  
260 265 270

Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln  
275 280 285

Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe  
290 295 300

Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu  
305 310 315 320

Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp  
325 330 335

Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly  
340 345 350

Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp  
355 360 365

Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu  
370 375 380

Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln  
385 390 395 400

Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly  
405 410 415

Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu  
420 425 430

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly  
435 440 445

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
450 455 460

<210> 50  
<211> 1392  
<212> DNA  
<213> Unknown

<220>  
<223> Cys (-) APAO; removal of cysteines 359 and 461

<220>  
<221> CDS  
<222> (1)...(1392)  
<223>

<400> 50  
aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt 48  
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly  
1 5 10 15

ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt 96  
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val  
20 25 30

ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg 144  
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser  
35 40 45

ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat		192	
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn			
50	55	60	
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg		240	
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu			
65	70	75	80
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa		288	
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln			
85	90	95	
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag		336	
Asp Gly Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu			
100	105	110	
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg		384	
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu			
115	120	125	
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag		432	
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys			
130	135	140	
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac		480	
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn			
145	150	155	160
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc		528	
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu			
165	170	175	
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc		576	
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile			
180	185	190	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc		624	
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly			
195	200	205	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tcg cat gcc		672	
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala			
210	215	220	
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc		720	
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val			
225	230	235	240
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg		768	
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser			
245	250	255	
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc		816	
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr			
260	265	270	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa		864	
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln			
275	280	285	

gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc		912	
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe			
290	295	300	
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc		960	
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu			
305	310	315	320
caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac		1008	
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp			
325	330	335	
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga		1056	
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly			
340	345	350	
cg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg		1104	
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp			
355	360	365	
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag		1152	
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu			
370	375	380	
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa		1200	
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln			
385	390	395	400
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt		1248	
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly			
405	410	415	
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag		1296	
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu			
420	425	430	
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt		1344	
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly			
435	440	445	
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag		1392	
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala			
450	455	460	
<210> 51			
<211> 463			
<212> PRT			
<213> Unknown			
<220>			
<223> Cys (-) APAO; removal of cysteines 359 and 461			
<400> 51			
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly			
1	5	10	15

Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val  
20 25 30

Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser  
35 40 45

Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn  
50 55 60

Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu  
65 70 75 80

Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln  
85 90 95

Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu  
100 105 110

Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu  
115 120 125

Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys  
130 135 140

Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn  
145 150 155 160

Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu  
165 170 175

Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile  
180 185 190

Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly  
195 200 205

Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala  
210 215 220

Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val  
225 230 235 240

Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser  
245 250 255

Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr  
260 265 270

Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln  
275 280 285

Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe  
290 295 300

Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu  
305 310 315 320

Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp  
325 330 335

Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly  
340 345 350

Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp  
355 360 365

Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu  
370 375 380

Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln  
385 390 395 400

Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly  
405 410 415

Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu  
420 425 430

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly  
435 440 445

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
450 455 460

<210> 52  
<211> 1392  
<212> DNA  
<213> Unknown

<220>  
 <223> Cys (-) APAO; removal of cysteines 169, 359, and 461

<220>  
 <221> CDS  
 <222> (1)...(1392)  
 <223>

<400>	52													
aaa gac aac gtt	gct	gac	gtg	gtg	gtg	ggc	gct	ggc	ttg	agc	ggt		48	
Lys Asp Asn Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly		
1	5			10				15						
ttg gag acg gca cgc	aaa	gtc	cag	gcc	gcc	ggt	ctg	agc	tcc	ctc	gtt		96	
Leu Glu Thr Ala Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Ser	Leu	Val			
20		25				30								
ctt gag gcg atg gat	cgt	gta	ggg	gga	aag	act	ctg	agc	gta	caa	tcg		144	
Leu Glu Ala Met Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser			
35		40			45									
ggc ccc agg acg act	atc	aac	gac	ctc	ggc	gct	gcf	tgg	atc	aat		192		
Gly Pro Gly Arg Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn			
50		55			60									
gac agc aac caa agc	gaa	gta	tcc	aga	ttg	ttt	gaa	aga	ttt	cat	ttg		240	
Asp Ser Asn Gln Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu			
65		70		75		80								
gag ggc gag ctc cag	agg	act	gga	aat	tca	atc	cat	caa	gca	caa		288		
Glu Gly Glu Leu Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln			
85		90			95									
gac ggt aca acc act	aca	gct	cct	tat	ggt	gac	tcc	ttg	ctg	agc	gag		336	
Asp Gly Thr Thr Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu					
100		105			110									
gag gtt gca agt gca	ctt	gct	ggc	gaa	ctc	ctc	ccc	gta	tgg	tct	cag	ctg		384
Glu Val Ala Ser Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu			
115		120			125									
atc gaa gag cat agc	ctt	caa	gac	ctc	aag	gcf	agc	cct	cag	gcf	aag		432	
Ile Glu His Ser Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys				
130		135			140									
cgf ctc gac agt gtg	agc	ttc	gcf	cac	tac	tgt	gag	aag	gaa	cta	aac		480	
Arg Leu Asp Ser Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn			
145		150			155			160						
ttg cct gct gtt ctc	ggc	gta	gca	aac	cag	atc	aca	cgc	gct	ctg	ctc		528	
Leu Pro Ala Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu			
165			170			175								
ggt gtg gaa gcc cac	gag	atc	agc	atg	ctt	ttt	ctc	acc	gac	tac	atc		576	
Gly Val Glu Ala His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile			
180		185			190									
aag agt gcc acc ggt	ctc	agt	aat	att	ttc	tcg	gac	aag	aaa	gac	ggc		624	
Lys Ser Ala Thr Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly			

195

200

205

ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tcg cat gcc Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala 210	215	220	672	
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val 225	230	235	240	720
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser 245	250	255	768	
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc Gly Ala Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr 260	265	270	816	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln 275	280	285	864	
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe 290	295	300	912	
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu 305	310	315	320	960
caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac Gln Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp 325	330	335	1008	
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly 340	345	350	1056	
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp 355	360	365	1104	
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu 370	375	380	1152	
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln 385	390	395	400	1200
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly 405	410	415	1248	
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu 420	425	430	1296	
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt			1344	

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly  
435 440 445

caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag 1392  
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
450 455 460

<210> 53  
<211> 463  
<212> PRT  
<213> Unknown

<220>  
<223> Cys (-) APAO; removal of cysteines 169, 359, and 461

<400> 53

Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly  
1 5 10 15

Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Ser Leu Val  
20 25 30

Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser  
35 40 45

Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn  
50 55 60

Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu  
65 70 75 80

Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln  
85 90 95

Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu  
100 105 110

Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu  
115 120 125

Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys  
130 135 140

Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn  
145 150 155 160

Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu

165

170

175

Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile  
180 185 190

Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly  
195 200 205

Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala  
210 215 220

Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val  
225 230 235 240

Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser  
245 250 255

Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr  
260 265 270

Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln  
275 280 285

Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe  
290 295 300

Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu  
305 310 315 320

Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp  
325 330 335

Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly  
340 345 350

Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp  
355 360 365

Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu  
370 375 380

Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln  
385 390 395 400

Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly  
405 410 415

Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu  
420 425 430

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly  
435 440 445

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
450 455 460